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RESULT 15
s47647
s47647
s47647
nitric-oxide synthase (EC 1.14.13.39) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Species: Rattus norvegicus (Norway rat)
C:Species: Rattus norvegicus (Norway rat)
C:Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000
C:Accession: $47647; JC1472
R:Geng, Y: Almqvist, M: Hansson, G.K.
Biochim. Biophys. Acta 1218, 421-424, 1994
A:Title: CDNA cloning and expression of inducible nitric oxide synthase from rat vascula A:Reference number: $47647; MUID:94325351; PMID:7519448
A:Residues: 1-1147 <GENN
A:Residues: 1-1147 <GENN
A:Residues: 1-1147 <GENN
A:Residues: 1-1147 <GENN
A:Cross-references: EMBL:X76881; NID:943283; PIDN:CAA54208.1; PID:9439284
R:Nunokawa, Y: Ishida, N: Tanaka, S.
Biochem. Biophys. Res. Commun. 191, 89-94, 1993
A:Title: Cloning of inducible nitric oxide synthase in rat vascular smooth muscle cells. A:Reference number: TC1472; MUID:93191721; PMID:7680561
A:Residues: 1-71, Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845-10, A:Residues: 1-71, 'Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845-10, A:Residues: 1-71, 'Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845-10, A:Residues: 1-71, 'Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845-10, A:Residues: 1-71, 'Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845-10, A:Residues: 1-71, 'Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845-10, A:Residues: 1-71, 'Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845-10, A:Residues: 1-71, 'Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845-10, A:Residues: 1-71, 'Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845-10, A:Residues: 1-71, 'Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845-10, A:Residues: 1-71, 'Y', 73-347, 'PV', 73-74, 'PV', 73-74, 'PV', 73-74, 'PV', 73-74, 'PV', 73-74, 'PV',
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Search completed: January 30, 2003, 14:38:54 Job time: 18 secs
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Best Local S
Matches 7
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Best Local Similarity 50.0
Matches 7; Conservative
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protein F52C12.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: F88640
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9951916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: F88640
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1453 <STO>
A;Cross-references: GB:chr_IV; PIDN:AAC68958.1; PID:g3800950; GSPDB:GN00022; CESP:F52C12
A;Map position: 4
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AB4567
AB45687
AB45687
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana, C.Y.; Species: A.; Species: A.; Shen, M.I.; Town, C.D.; Fujii, C.Y.;
R.; Klin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A.;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Rocession: A84567
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A;Roseidues: 1-126 <STO>
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A;Roseidues: 1-126 <STO>
A;Roseidues:
probable DNA methylase STY1014 [imported] - Salmonella enterica subsp. enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 02-Aug-2002 C;Accession: AF0617 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; C
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           Churcher
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C; Function:
A; Description:
C; Superfamily:

catalyzes the oxidation of an L-arginine guanidino nitrogen and of nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein

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A; Status: pretamana, A; Molecule type: mRNA A; Residues: 1-1144 (XIE) A; Residues: 1-1144 (XIE) A; Residues: 1-124 (XIE) A; Cross-references: GB:M87039; NID:g198406; PIDN:AAA39315.1; PID:g198407 A; Cross-references: GB:M87039; NID:g198406; PID:AAA39315.1; PID:g198407 A; Cross-references: GB:M87039; NID:g198406; PID:AAA39315.1; PID:g198407 A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide A; Title: Molecular cloning and functional expression of an inducible nitric oxide and functional expression oxide and
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A; Authors: Parry, C.; Quail, M.; Rutherford, K.; A; Atthors: Parry, C.; Quail, M.; Rutherford, K.; A; Title: Complete genome sequence of a multiple A; Title: Complete genome sequence of a multiple A; Title: Complete A; B0502; PMID:11677608
                                                                       A; Nolecule type: mRNĀ
A; Molecule type: mRNĀ
A; Hesidues: 1-190,'V',192-765,'P',767-843,'G',845-1144 <LOW>
A; Residues: 1-190,'V',192-765,'P',767-843,'G',845-1144 <LOW>
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A; Cross-references: GB:M92649; NID:9200109
A; Experimental source: BALB/C, RAW 264.7 cells, macrophage
A; Experimental source: BALB/C, RAW 264.7 cells, macrophage
A; Experimental source: MALB/C, RAW 264.7 cells, macrophage
A; Experimental source: BALB/C, RAW 264.7 cells,
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A;Title: Cloned and expressed macrophage nitric oxide synthase A;Reference number: A46186; MUID:92357701; PMID:1379716
A;Accession: A46186
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A; Residues: I-1144 < LYO>
A; Residues: GB:M84373; NID:g200095; PIDN:AAA39834.1; PID:g200096
A; Cross-references: GB:M84373; NID:g200095; PIDN:AAA39834.1; PID:g200096
R; Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.
Blochem. Biophys. Res. Commun. 191, 767-774, 1993
Blochem. Biophys. Res. Commun. 191, 767-774, 1993
A; Title: Hepatocytes and macrophages express an identical cytokine induc.
A; Reference number: JN0457; MUID:93221515; PMID:7682072
A; Accession: JN0458
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: A43271; A42166; JN0458; A46186
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A; Accession: AF0617
A; Status: preliminary
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C; Superfamily:
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A; Residues: 1-293 < PAR>
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A; Residues: 1-278, 'F', 280-682, 'H', 684-937, 939-1144 <WOO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent - mouse
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A; Gene: NOS
                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; not compared with conceptual translation
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hypothetical protein DKFZp434L0850.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C:Accession: T42699; 73459
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, November 1999
A:Reference number: Z22232
A:Accession: T42699
A:Accession: T42699
A:Coss-references: EMBL:AL133042
A:Experimental source: adult testis; clone DKFZp434L0850
R:Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, October 1999
A:Reference number: Z21540
A:Accession: T34559
A:Status: preliminary
A:Molcule type: mRNA
A:Residues: 1-303 <POU>
A:Residues: 1-303 <POU>
A:Cross-references: EMBL:AL122038
A:Experimental source: adult testis; clone DKFZp43410850
C:Genetics:
A;Note: DKFZp434L0850.1
                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 90, 11419-11423, 1993

A.Title: Cloning, characterization, and expression of a cDNA encoding an inducible nit A; Reference number: A49676; MUID:94068614; PMID:7504305

A. Accession: A49676
A;Molecule type: mRNA
A;Residues: 1-607, 'L',609-1153 <PAR>
A;Residues: 1-607, 'L',609-1153 <PAR>
A;Coss-references: EMBL:U31511; NID:g951320; PIDN:AAB49041.1; PID:g951321
R;Guo, F.H.; De Raeve, H.R.; Rice, T.W.; Stuehr, D.J.; Thunnissen, F.B.; E.
Proc. Natl. Acad. Sci. U.S.A. 92, 7809-7813, 1995
A;Title: Continuous nitric oxide synthesis by inducible nitric oxide synth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nitric-oxide synthase (EC 1.14.13.39), inducible - human c;Speciles: Homo sapiens (man) c;Speciles: Homo sapiens (man) C;Date: 16:Feb-1996 ##sequence_revision 16:Feb-1996 #text_change 20-Jun-2000 C;Accession: A49676; JX0345; G01947; I38933; S47566; A47475 R;Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; H.R.; Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; H.R.; Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; H.R.; Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; H.R.; Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; H.R.; Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; H.R.; Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; H.R.; Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; H.R.; Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; H.R.; Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; H.R.; Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; H.R.; Charles, I.G.; Palmer, R.M.; H.R.; Palmer, R.M.; H.R.; Palmer, R.M.; Palmer,
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F:539-1127/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:541-677/Domain: flavodoxin homology <FEXP
F:623-654/Region: FMN binding #status predicted
F:765-778/Region: FMD-pyrophosphate binding #status predicted
F:903-913/Region: FAD-150alloxazine binding #status predicted
F:903-913/Region: NADP-ribose binding #status predicted
F:1076-1091/Region: NADP-adenine binding #status predicted
F:1076-1091/Region: NADP-adenine binding #status predicted
F:200/Binding site: heme iron (Cys) (axial ligand) #status predict.
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A;Nolecule type: mRNA
A;Residues: 1-422,'I',424-804,'D',806-830,'SP',833-932,'G',934-965,'A',967-986,'V'
A;Residues: 1-422,'I',424-804,'D',806-830,'SP',833-932,'G',934-965,'A',967-986,'V'
A;Cross references: GB:L09210; NID:g292241; PIDN:AAA59171.1; PID:g292242
A;Experimental source: hepatocytes
A;Note: sequence extracted from NCBI backbone (NCBIP:129733)
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A; Residues: 1-22, 'G', 4-153, 'L', 155-176, 'V', 178-799, 'A', 801-912, 'p', 914-1153 <MAI>
A; Residues: 1-22, 'G', 4-153, 'L', 155-176, 'V', 178-799, 'A', 801-912, 'p', 914-1153 <MAI>
A; Cross-references: EMBL:U05810; NID:g452487; PIDN:AAA56666.1; PID:g452488
R; Geller, D.A.; Lowenstein, C.J.; Shapiro, R.A.; Nussler, A.K.; Di Silvio, M.; Wang,
Proc. Natl. Acad. Sci. U.S.A. 90, 3491-3495, 1993
A; Title: Molecular cloning and expression of inducible nitric oxide synthase from hur
A; Reference number: A47475; MUID:93234523; PMID:7682706
                                                                                                                                                                                                       R;Cachon-Gonzalez, M.B.; Fenner, S.; Coffin, J.M.; Moran, C.; Best, Proc. Natl. Acad. Sci. U.S.A. 91, 7717-7721, 1994
A;Title: Structure and expression of the hairless gene of mice.
A;Reference number: I48378; MUID:94329587; PMID:8052649
A;Accession: I48378
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                       hairless protein - mouse
C;Speckes: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I48378
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I48378
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A;Cross-references: GDB:139215;
A;Map position: 17cen-17q11.2
C;Function: Catalyzes the oxi
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Biochim. Biophys. Acta 1208, 145-150, 1994
A;Title: Inducible nitric oxide synthase from human articular chondrocytes: cDNA clon
A;Reference number: S47566; MUID:94368816; PMID:7522054
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A; Accession: I38933
A; Status: preliminary; nucleic acid sequence not shown; tran:
A; Molecule type: mRNA
A; Residues: 1-675, 'I', 677-932, 'G', 934-965, 'A', 967-1153 < RE2>
                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-1182 <RES>
A; Cross-references: EMBL
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8; Conser
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A; Cross-references: EMBL: X56685; NID: g117; PIDN: CAA40014.1; PID: g118 A; Note: part of this sequence, including the amino end of the mature R; Henner, W.D.; Kiker, N.P.; Jorgensen, T.J.; Munck, J.N. Nucleic Acids Res. 15.5529-5544, 1987
A; Title: Purification and amino-terminal amino acid sequence of an ap A; Reference number: S30761; MUID: 87289027; PMID: 2441359
A; Recession: S30761
A; Molecule type: protein A; Molecule type: protein A; Residues: C-20, 'LP', 23 <HEN>C; Superfamily: exodeoxyribonuclease III
C; Keywords: Carbon-Oxygen lyase; DNA repair; endonuclease; nucleus F; 2-318/Product: DNA-(apurinic or apyrimidinic site) lyase #status pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - bovine N;Alternate names: apurinic/apyrimidinic endonuclease I; BAP-1 protein C;Species: Bos primigenius taurus (cattle) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Feb-2000 C;Accession: S26830; S30761
                                                                                                                                                                                                                                                                             R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Haglus, S.; O'Cal Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen A;Reference number: AD3252; PMID:11756688
A;Accession: AI3600
A;Status: preliminary
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A;Title: Isolation of cDNA clones encoding an enzyme from bovine cells that repairs A;Reference number: S26830; MUID:91212189; PMID:1708495
A;Accession: S26830
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C;Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
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A; Residues: 1-318 < ROB>
                                                                                                                                          A; Gene: BMEII0730
                                                                                                                                                                                            A; Experimental source:
                                                                                                                                                                                                                A;Residues: 1-328 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53972.1; PID:g17984919; GSPDB:GN00191
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Pred. No. 5.9e-05;
Score
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R;Meurer, G.; Biermann, G.; Schuetz, A.; Harth, S.; Schweizer, Mol. Gen. Genet. 232, 106-116, 1992 A;Title: Molecular structure of the multifunctional fatty acid he two yeast genes FASI and FAS2.
A;Reference number: S20473; MUID:92204122; PMID:1552898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Evidence for lateral gene transfer between Archaea A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: C72293
                                                                                                           A;Start codon: GTG
C;Superfamily: Brevibacterium ammoniagenes
C;Keywords: acyltransferase; coenzyme A
                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-1430,'V',1432-3104 <SCH>
A;Cross-references: EMBL:X64795; NID:g39319; PIDN:CAA46024.1; PID:g580746
                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, December A; Reference number: S28645
                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: S20473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fatty-acid synthase (EC 2.3.1.85) - Brevibacterium ammoniagenes C;Species: Brevibacterium ammoniagenes C;Decies: Brevibacterium ammoniagenes C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 05-May-2000 C;Accession: S20473; S28645
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C;Superfamily: Thermotoga maritima hypothetical protein
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A; Residues: 1-612 <ARN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: C72293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C72293
                                                                                                                                                                     A; Gene:
                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                          A; Accession:
                                                                                                                                                                                                                                                              A; Reference number: A; Accession: S28645
                                                                                                                                                                                                                                                                                                                  R;Schweizer,
                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: X64795
                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-3104 <MEU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE001770; GB:AE000512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Nelson, K.E.; Clayton, R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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1 AAGEGPALYEDPPD 14
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9; Conser
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                                    Similarity
9; Conserv
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75.0%;
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Cotton, M.D.;
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                                      0
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                                                     Score 43;
Pred. No.
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; Pratt, M.S.;
                                                                                                                                 fatty-acid
                                      1.6e+02;
ches 5;
                                                                           DВ
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                                                                           Length 3104;
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; Phillips, C.A.; Richardson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetase gene of
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AISGGPALYERPVD

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A:Residues: 1-50,'H',52-318 <SEK>
A:Cross*references: DDBJ:D13370; NID:g219473; PIDN:BAA02633.1; PID:g219474
A:Cross*references: DDBJ:D13370; NID:g219473; PIDN:BAA02633.1; PID:g219474
B:A:Ata 1219, 15-25, 1994
A:Title: Structure, promoter analysis and chromosomal assignment of the human A:Reference number: S47521; MUID:94368844; PMID:8086453
A:Accession: S47521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 2-21,'p',23-26 <DEM2>
A;Residues: 2-21,'p',23-26 <DEM2>
A;Residues: 2-21,'p',23-26 <DEM2>
R;Barzilay, G.; Walker, L.J.; Robson, C.N.; Hickson, I.D.
Nucleic Acids Res. 23, 1544-1550, 1995
A;Title: Site-directed mutagenesis of the human DNA repair enzyme HAP1: identification A;Reference number: S55547; MUID:95303638; PMID:7784208
A;Accession: S55547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R:Robson, C.N.; Hickson, I.D.
Nucleic Acids Res. 19, 5519-5523, 1991
A;Title: Isolation of cDNA clones encoding A;Reference number: S34422; MUID:92051291; A;Accession: S34422
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A; Residues: 1-147, 'E',149-318 < AKI>
A; Residues: 1-147, 'E',149-318 < AKI>
A; Cross-references: DDBJ:D13370; NID:9219473; PIDN:BAA02633.1; PID:9219474
A; Cross-references: DDBJ:D13370; NID:9219473; PIDN:BAA02633.1; PID:9219474
R; Harrison, L.; Ascione, G.; Menninger, J.C.; Ward, D.C.; Demple, B.
Hum. Mol. Genet. 1, 677-680, 1992
                                                                                 ₽
                                                                                                                             ð
                                                                                                                                                                                                                                                                                                  F:2-318/Product: DNA-(apurinic or apyrimidinic site) F:96/Binding site: magnesium (Glu) #status predicted F:309/Active site: His #status predicted
                                                                                                                                                                                                                                                                                                                                                          C;Keywords: carbon-oxygen lyase; DNA repair; endonuclease; magnesium; nucleus F;2-318/Product: DNA-(apurinic or apyrimidinic site) lyase 1 #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Pathway: DNA repair C; Superfamily: exodeoxyribonuclease III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GDB:129088;
A; Map position: 14q11.2-14q12
A; Introns: 20/1; 82/3; 147/1
A; Note: the list of introns may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Demple, B.; Herman, T.; Chen, D.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 11450-11454, 1991
A;Title: Cloning and expression of APE, the cDNA encoding
A;Reference number: A41631; MUID:92107988; PMID:1722334
A;Accession: A41631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA, A; Residues: 1-336,'A',238-318 <RO2>
A; Residues: 1-336,'A',238-318 <RO2>
A; Cross-references: EMBL:X59764; NID:g32023; PIDN:CAA42437.1;
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A;Residues: 1-146 <HAR>
A;Cross-references: GB:M99703; NID:g178748; PIDN:AAA58373.1; PID:g553182
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A; Reference number: I39472;
A; Accession: I39472
RESULT 2
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A;Residues: 1-56,'A',58-305,'A',307-318 <DEM1>
A;Cross-references: GB:M80261; NID:g178742; PIDN:AAA58371.1;
A;Accession: B41631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: catalyzes endonucleolytic cleavage near apurinic or apyrimidinic
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                                                                                                                                                                                             Matches
                                                                                 37
                                                                                                                                                                                                                          Local
Local
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                                                                                                                                     AAGEGPALYEDPPD 14
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                                                                              AAGEGPALYEDPPD
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                                                                                                                                                                                             0;
                                                                                                                                                                                       Score 78; DB 2;
Pred. No. 1.2e-05;
Mismatches 0;
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                                                                                                                                                                                                                                              Length 318;
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A;Note: part of this sequence, including the amino end of the mature protein, was con R;Seki, S.; Ikeda, S.; Watanabe, S.; Hatsushika, M.; Tsutsui, K.; Akiyama, K.; Zhang, Biochim. Biophys. Acta 1079, 57-64, 1991
A;Title: A mouse DNA repair enzyme (APEX nuclease) having exonuclease and apurintc/ap A;Reference number: S17524; MUID:91363416; PMID:1716153
A;Accession: S17524
                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-317 <R
                                                                                                                                                                                                                                                                                                                                R; Takiguchi, Y.; Chen, D.J.
Mamm. Genome 5, 717-722, 1994
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A; Residues: 1-18 < AKI>
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A; Residues: 1-316 <WIL>
                                                 A;Cross-references: MGI:88042
                                                                                                                                     A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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A; Residues: 1-317 <SEK>
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Best Local
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13; Conserv
exodeoxyribonuclease
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                                                                                                                                                                  <RES>
                                                                                                                                     EMBL:U12273; NID:g533107; PIDN:AAC13769.1;
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R:Wilson, T.M.; Carney, J.P.; Kelley, M.R. Nucleic Acids Res. 22, 530-531, 1994
A:Title: Cloning of the multifunctional rat A;Reference number: $42397; MUID:94173709; PA;Accession: $42397.
                                                                                                                                                                                                                                                                                                                                                                             DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - W.Alternate names: apurinic/apyrimidinic endonuclease C:Species: Rattus norvegicus (Norway rat) C:Date: 20-Cct-1994 #sequence_revision 10-Nov-1995 #text_cl C:Accession: S42397
                                                                                                      A;Cross-references: GB:L27076; NID:9468370; PIDN:AAA21019.1; PID:9468371 C;Superfamily: exodeoxyribonuclease III C;Keywords: carbon-oxygen lyase; DNA repair; endonuclease; nucleus
                            Score 74; I
Pred. No. 5
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  10-Nov-1995 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                            b apurinic/apyrimidinic endonuclease
pmID:7510394
                                                         DB
                            8e-05;
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DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - mouse N;Alternate names: apurinic/apyrimidinic endonuclease; desoxyribonuclease C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Jun-2000 C;Accession: A39500; S17524; A56747; I49098; JU0372 R;Seki, S.; Akiyama, K.; Watanabe, S.; Hatsushika, M.; Ikeda, S.; Tsutsui, K. J. Biol. Chem. 266, 20797-20802, 1991 A;Title: CDNA and deduced amino acid sequence of a mouse DNA repair enzyme (APEX nucl A;Reference number: A39500; MUID:92041936; PMID:1939131 A;Accession: A39500

R;Aklyama, K.; Nagao, K.; Oshida, T.; Tsutsui, K.; Yoshida, M.C.; Seki, S. Genomics 26, 63-69, 1995
A;Title: Cloning, sequence analysis, and chromosomal assignment of the mouse A;Reference number: A56747; MUID:95301294; PMID:7782087
A;Accession: A56747 Apex

gen

A;Title: Genomic structure of the mouse apurinic/apyrimidinic endonuclease gene. A;Reference number: I49098; MUID:95178846; PMID:7533013
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000 C;Accession: S23550; S25570; S35454; S35456; S23935; S47521; I39472; S34422; A41631; R;Xanthoudakis, S.; Miao, G.; Wang, F.; Pan, Y.C.E.; Curran, T. EMBO J. 11, 3323-3335, 1992

A; Title: Redox activation of Fos-Jun DNA binding activity is mediated by a DNA repair A; Reference number: S23550; MUID:92371440; PMID:1380454

A; Accession: S23550

A; Molecule type: mRNA; protein

A;Cross-references: GB:S43127; NID:g254068; PIDN:AAB22977.1; PID:g254069
A;Note: part of this sequence, including the amino end of the mature protein, was det R;Robson, C.N.; Hochhauser, D.; Craig, R.; Rack, K.; Buckle, V.J.; Hickson, I.D. Nucleic Acids Res. 20, 4417-4421, 1992
A;Title: Structure of the human DNA repair gene HAP1 and its localisation to chromoso A;Reference number: S25570; MUID:93027134; PMID:1383925
A;Accession: S25570

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-318 <ROB>

A;Cross-references: EMBL:X66133; NID:g32021; PIDN:CAA46925.1; PID:g32022
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1992
R;Cheng, X.B.; Bunville, J.; Patterson, T.A.
Nucleic Acids Res. 20, 370, 1992

A;Title: Nucleotide sequence of a CDNA for an apurinic/apyrimidinic endonuclease from A;Reference number: S35454; MUID:92158631; PMID:1371347

A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Accession: S35454

A; Molecule type: mRNA A; Residues: 1-318 < CHE>

A;Cross-references: EMBL:M81955; NID:g178746; PIDN:AAA58372.1; PID:g178747
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R;Zhao, B.; Grandy, D.K.; Hagerup, J.M.; Magenis, R.E.; Smith, L.; Chauhan, B.C.; Hen Nucleic Acids Res. 20, 4097-4098, 1992
A;Title: The human gene for apurinic/apyrimidinic endonuclease (HAP1): sequence and 1 A;Reference number: S35456; MUID:92375705; PMID:1380694
A;Accession: S35456

A;Status: preliminary

A; Molecule type: DNA A; Residues: 1-318 <ZHA>

A;Cross-references: EMBL:M92444; NID:g183779; PIDN:AAAS8629.1; PID:g183780 R;Sek1, S.; Hatsushika, M.; Watanabe, S.; Akiyama, K.; Nagao, K.; Tsutsui, K. Blochim. Biophys. Acta 1131, 287-299, 1992 A;Title: cDNA cloning, sequencing, expression and possible domain structure of human A;Reference number: S23935; MUID:92329542; PMID:1627644 A;Accession: S23935

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ALIGNMENTS

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APE1_HUMAN STANDARD; PRT; 317 AA. P27695; Q99775; Q969L5; Q1-AUG-1992 (Rel. 23, Created) Q1-AUG-1992 (Rel. 23, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) DNA-(apurinic or apyrimidinic site) lysse (EC endonuclease 1) (APEX nuclease) (APEN) (REF-1 APEX OR APE OR HAP1 OR REF1 OR APX.
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"Isolation of cDNA clones encoding a human apurinic/apyrimidinic endonuclease that corrects DNA repair and mutagenesis defects in coli xth (exonuclease III) mutants.";
Nucleic Acids Res. 19:5519-5523(1991).
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MEDLINE=92375705; PubMed=1380694;

Zhao B. Grandy D.K., Hagerup J.M., Magenis R.E., Smith L.,

Chauhan B.C., Henner W.D.;

"The human gene for apurinic/apyrimidinic endonuclease (HAPI):

sequence and localization to chromosome 14 band q12.";

Nucleic Acids Res. 20:4097-4098(1992).
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MEDLINE-93371440; PubMed-1380454;

Xanthoudakis S., Wang F., Pan Y.-C.E., Curran T.;

Redox activation of Fos-Jun DNA binding activity is mediated DNA repair enzyme.";

DNA repair enzyme.";
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MEDLINE-92051291; PubMed-1719477;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hickson I.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                     Biophys. Acta 1131:287-299(1992).
                                                                                                                                                                                                          PubMed=1627644;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAP1
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MEDLINE=94368844; PubMed-8086453; Akiyama K., Seki S., Oshida T., Yoshida M.; "Structure, promoter analysis and chromosomal assignment of the human APEX gene.";

Biochim.

gene.

restrictions on for

ch/announce/

collaboration

outstation 1n

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Cheng X.B., Bunville J., Patterson T.A.
"Nucleotide sequence of a cDNA for an
endonuclease from HeLa cells.";
Nucleic Acids Res. 20:370-370(1992).
[9]
                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 31-317.

MEDLINE-98063001; PubMed-9351835;

GORMAN A., Morera S., Rothwell D.G., de La Fortelle E., Mol C.I

Tainer J.A., Hickson I.D., Freemont P.S.;

"The crystal structure of the human DNA repair endonuclease HAP1
suggests the recognition of extra-helical deoxyribose at DNA abases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu W., Andersson B., Worley K.C., Muzny D.M., Din
Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs
"Large-scale concatenation cDNA sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92107968; PubMed-1722334; Demple B., Herman T., Chen D.S.; Chen coloning and expression of APE, the cDNA encoding the major appurinic endonuclease: definition of a family of DNA repair
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97086686; PubMed=8932375;
Rothwell D.G., Hickson I.D.;
"Asparagine 212 is essential for abasic site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harrison L., Ascione G., Menninger "Human apurinic endonuclease gene ("Human apurinic endonuclease gene (mapping (chromosome 14g11.2-12)."; Hum. Mol. Genet. 1:677-680(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-92158631;
                                                                                                                                                                                                                                       human apurinic/apyrimidinic endonuclease, catalytic mechanism.";
J. Mol. Biol. 307:1023-1024/^^^
                                                                                                                                                                                                                                                                                                                   Beernink P.T., S
Wilson D.M. III,
                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
MEDLINE=21184546; PubMed=11286553;
                               X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS)
MEDLINE=20129262; PubMed=10667800;
Mol C.D., Izumi T., Mitra S., Tainer J
                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGENESIS OF ASN-211
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                                                                                                   <u>емво J. 16:6548-6558(1997).</u>
                                                                                                                                                                                                                                                                                                                                                                                                   repair endonuclease HAP1.";
leic Acids Res. 24:4217-4221(1996).
repair and coordination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A.
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                 structures
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               itra S., Tainer J.A.; and mutants reveal a
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(APE):
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                   abasic DNA binding
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structure
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bbs R.A.;
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                   APE1
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      EMBL; X6613; CAA46925.1; -.
EMBL; X59764; CAA42437.1; -.
EMBL; M59704; AAA58629.1; -.
EMBL; M99703; AAA58373.1; -.
EMBL; D90373; BAA14381.1; -.
EMBL; D13370; BAA053371.1; -.
EMBL; M80261; AAA58371.1; -.
EMBL; M81955; AAA58372.1; -.
EMBL; U79268; AAA58372.1; -.
EMBL; BC002338; AAH02338.1; -.
EMBL; BC0024979; AAH02979.1; -.
EMBL; BC000145; AAH02979.1; -.
EMBL; BC000147; AAH19291.1; -.
EMBL; BC001291; AAH19291.1; -.
EMBL; BC001291; AAH19291.1; -.
EMBL; S43127; AAB22977.1; -.
                                                                                                                                                                                                                                     InterPro; IPR000097; APendonclsel.
InterPro; IPR004442; EXDNASe_III.
InterPro; IPR004442; EXDIII xth.
InterPro; IPR005135; Exo_endo_phos.
InterPro; IPR005135; Exo_endo_phos.
ITGREAMS; TIGR00195; exoDNASe_III; 1.
TIGREAMS; TIGR00633; xth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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1- FUNCTION: REPAIRS OXIDATIVE DNA DAMAGES IN VITRO. MAY HAVE A ROLE IN PROPECTION AGAINST CELL LETHALITY AND SUPPRESSION OF MUTATIONS. REMOVES THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA STRAND BREAKS GENERATED BY IONIZING RADIATIONS AND BLEOMYCIN.

1-- CATALYTIC ACTIVITY: The C-O-P bond 3' to the appurinic or apyrimidinic site in DNA is broken by a beta-elimination reaction, leaving a 3' terminal unsaturated sugar and a product with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR;
PIR;
PIR;
PIR;
                   METAL
METAL
METAL
METAL
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ACT_SITE
VARIANT
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Genew; HGNC:587; l
MIM; 107748;
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PDB;
PDB;
PDB;
PDB;
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                                                                                                                                                                      PROSITE; PS00726; AP_NUCLEASE_F1_1; PROSITE; PS00727; AP_NUCLEASE_F1_3; PROSITE; PS00728; AP_NUCLEASE_F1_3; DNA repair; Lyase; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A41631; A41631.
JU0373; JU0373.
S22072; S22072; S22550; S23550.
S23935; S23935; S23935.
S235456; S35456; S35454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       terminal 5'-phosphate.
SUBUNIT: MONOMER.
SUBCELLULAR LOCATION: N
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1E9N;
1HD7;
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16-FEB-01.
16-FEB-01.
02-FEB-00.
02-FEB-00.
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67
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TO THE AP/EXOA FAMILY OF DNA REPAIR ENZYMES.
                                  MAGNESIUM OR N
                   GENERAL
Q -> H (
        /FTId=VAR_013455
                   ESIUM OR MANGANESE.
LIL DASE (BY SIMILARITY).
H. (IN DESNP:1048945).
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; 1.
; Polymorphism; :
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"DNA-bound

Submitted Strausberg Genome

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                                characterization.";

Blochim. Biophys. Acta 1079:57-64(1991).

-i. FUNCTION: REPAIRS OXIDATIVE DNA DAMAGES IN VITRO. MAY HAVE A ROLE IN PROTECTION AGAINST CELL LETHALITY AND SUPPRESSION OF MUTATIONS. REMOVES THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA STRAND BREAKS GENERATED BY IONIZING RADIATIONS AND BLEOMYCIN.

-i. CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or apyrimidinic site in DNA is broken by a beta-elimination reaction, leaving a 3'-terminal unsaturated sugar and a product with a terminal 5'-phosphate.

-i. SUBURIT: MONOBER (BY SIMILARITY).

-i. SUBCELLULAR LOCATION: NUCLEAR.

-i. SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                  *Cloning, sequence analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seki S., A)
Tsutsui K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC 1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-(apurinic or apyrimidinic site) lyase (EC endonuclease 1) (APEX nuclease) (APEN).
                                                                                                                                                                                                                                                                                                                                   MEDLINE-95301294; PubMed-7782087; Akiyama K., Nagao K., Oshida T., **Cloning, sequence analysis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "cDNA and deduced amino acid sequence of a (APEX nuclease) with significant homology exonuclease III.";
This SWISS-PROT entry between the Swiss Ins
                                                                                                                                                                                                      *A mouse DNA repair enzyme (APEX nuclease) having exonuclease and apurinic/apyrimidinic endonuclease activities: purification and
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BALB/C; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-92041936;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                              Seki S., Ikeda
                                                                                                                                                                                                                                                          MEDLINE-91363416; PubMed-1716153;
                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE OF 1-21,
                                                                                                                                                                                                                                                                                                                                                                                                                               gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-129; TISSUE-Embryo;
MEDLINE-95178846; PubMed-7533013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                           Genomics 26:63-69(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genomic structure of the mouse apurinic/apyrimidinic endonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takiguchi Y., Chen D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                             LOCATION: Nuclear.
BELONGS TO THE AP/EXOA FAMILY OF DNA REPAIR ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=1939131;
K., Watanabe S.,
Institute of Bioinformatics
                                                                                                                                                                                                                                              Watanabe
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Rodentia;
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                                                                                                                                                                                                                                                                                    CHARACTERIZATION
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produced through a collaboration -
atics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse DNA repair enzyme
to Escherichia coli
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the mouse
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RESULT 3
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Best Local S
Matches 13
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Interpro; IPR00097; APendoncisel.
Interpro; IPR004442; ExoDNase_III.
Interpro; IPR004403; ExOIII_xth.
Interpro; IPR004808; ExOIII_xth.
Interpro; IPR005135; Exo_endo_phos.
Pfam; PF03772; Exo_endo_phos.
TIGRFAMS; TIGR00195; exoDNase_III; 1.
TIGRFAMS; TIGR00195; exONase_III; 1.
PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
PROSITE; PS00727; AP_NUCLEASE_F1_2; 1.
PROSITE; PS00728; AP_NUCLEASE_F1_3; 1.
                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update
15-JUN-2002 (Rel. 41, Last annotation update
DNA-(apurinic or apyrimidinic site) lyase
endonuclease 1) (APEX nuclease) (APEN).
                                                                                                                                                                                                                                                                                    APE1_RAT
P43138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE SEQUENCE
                                                                    STRAIN-Sprague-Dawley; TISSUE-Testis; MEDLINE-94173709; PubMed-7510394; Wilson T.M., Carney J.P., Kelley M.R.; "Cloning of the multifunctional rat apuendonuclease (rAPEN)/redox factor from Nucleic Acids Res. 22:530-531(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D90374; BAA14382.1; -.
EMBL; U12273; AAC13769.1; -.
EMBL; D38077; BAA07270.1; -.
PIR; S17524; S17524.
PIR; A39500. A39500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
STRAIN-Sprague-Dawley: TISSUE-Brain; Tan Y., Aklyama K., Seki S., Tabayashi Submitted (DEC-1994) to the EMBL/GenBar [3]
                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Pred. No.
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CF899FA8182AA558 CRC64;
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OR SUBSTRATE ()
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Yao M., A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          processed beeudogene (Apexp1).";
submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
i- FUNCTION: REPAIRS OXIDATIVE DNA DAWAGES IN VITRO. MAY HAVE
IN PROFECTION AGAINST CELL LETHALITY AND SUPPRESSION OF MUT
REMOVES THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yao M., Akiyama K., Tan Y., Sarker A.H., Ikeda S., Alam Tsutsui K., Yoshida M.C., Seki S.; "Genomic structure of the rat Apex (major AP endonucleas an adjacent putative O-sialoglycoprotease (Prsmg1/Gcpl1)
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  endonuclease
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                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BREAKS GENERATED BY IONIZING RADIATIONS AND BLEOWICIN.
CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or apyrimidinic site in DNA is broken by a beta-elimination reaction, leaving a 3'-terminal unsaturated sugar and a product with a terminal 5'-phosphate.
SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELICULAR ICCATION: Nuclear.
SIMILARITY: BELONGS TO THE AP/EXOA FAMILY OF DNA REPAIR ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
by non-profit institutions as long as i
ified and this statement is not removed. Us
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                                                                                                                                    AAGEGPVLYEDPPD
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PS00727; AP_NUCLEASE_F1_2;
PS00728; AP_NUCLEASE_F1_3;
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IPR005135;
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(Rel. 20, Last sequence update)
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ic or apyrimidinic site) lyase (EC
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ExoIII_xth.
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MISSING (IN REF. 1).

R -> A (IN REF. 1).
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Pred. No.
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Henner W.D., Kiker N.P., Jorgensen T.J., Munck J.-N.;

Refere W.D., Kiker N.P., Jorgensen T.J., Munck J.-N.;

REMOVES THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA STRAND CONTROL OF THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA STRAND CONTROL OF THE DNA STRAND CONTROL OF THE DNA STRAND CONTROL OF CONTROL OF DOING 3' to the apurinic or apyrimidinic site in DNA is broken by a beta-elimination reaction, Control of the Monomer Market Sugar and a product with a terminal 5'-phosphate.

C. -I- SUBGURIT: MONOMER (BY SIMILARITY).

C. -I- SUBGURITAR LOCATION: Nuclear.

C. -I- SUBGURITAR LOCATION: Nuclear.

C. -I- SUBGURITAR SECRETAL DNA DAMAGING AGENTS.

C. -I- SUBGURITS: BELONGS TO THE AP/EXOA FAMILY OF DNA REPAIR ENZYMES.
Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Thymus;

MEDLINE-91212189; PubMed=1708495;

Robson C.N., Milne A.M., Pappin D.J.C.
Robson C.N., clones encoding an
                                                                                                                                                                                                                                                                                                                              EMBL; X56685;
PIR; S26830; S
HSSP; P27695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long or modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                   ACT_SITE CONFLICT SEQUENCE
                                                                                                                                                                                                PROSITE;
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Pfam; PF0
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MEDLINE=87289027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9913;
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TIGREAMS; TIGR00633; xth; 1
PROSITE; PS00726; AP_NUCLEASE_F1_1;
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                                                                                                                                                                                                PS00728;
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IPR004442; ExoDNase_III.
IPR004808; ExoIII_xth.
IPR005135; Exo_endo_phos.
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AP_NUCLEASE_F1_3;
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                 79.5%;
78.6%;
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                 Score 62;
Pred. No.
                                                                  MAGNESIUM
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ing an enzyme from bovine cells that
vitro: homology with bacterial repair
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AAGEGPALYEDPPD AVGEGAVLYEDPPD 49

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30-mAY-2000 (Rel. 39, Created)
30-mAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Nitric oxide synthase, inducible (EC 1.14.13.39)
(Inducible NOS) (INOS) (Fragment).
                                                                                                                                                                                                                                                                                                          PROSITE; PS60001; NOS; PAR' Oxidoreductase; NADP; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U59390; AAB40614.1; HSSP; P35228; 4NOS.
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Mammalia; Eutheria;
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98273497; PubMed-9613441;
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                                                                                                                                                                                                                                                                                     Multigene family.
                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02898; NO_synthase;
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TISSUE SPECIFICITY: DETECTED IN BOTH STIMULATED AND UNSTIMULATED IMMUNE CELLS AND MACROPHAGES WITH LITTLE OR NO UPREGULATION FOLLOWING CELLULAR STIMULATION WITH LIPOPOLYSACCHARIDES (LPS) OR CONCANAVALIN A (CONA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDUCTION: LITTLE BY LPS OR CONA IN SPLEEN CELLS. SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN SIMILARITY).
ADGRDPELFEIPPD 112
                                                                                                   Similarity
8; Conserv
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                                                                                                                                                                                                         215
215 AA;
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                        NOS; PARTIAL.
                                                                                                                                                                                                       215
24716 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                         53.8%;
                                                                                                                                                                                                                                                                                                          FMN; Calmodulin-binding;
                                                                                                Score 42; D
Pred. No. 5.
1; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                         FECFF5BD85B65808 CRC64;
                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215
                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₹
                                                                                                   5
                                                                                                                                                 Length 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOS,
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Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type
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RESULT

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RESULT
STM2_HU
ID MX
ID 10
ID 10
ID 11
ID 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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Q12630;
                                                                                                                                                                                                      Q9P246; Q9BQH2; Q9H8R1;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Stromal interaction molecule 2 precursor.
STIM2 OR KIAA1482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROY entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most proof it institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Analysis of a transketolase gene from Kluyveromyces lactis reveals that the yeast enzymes are more related to transketolases of prokaryotic origins than to those of higher eukaryotes.";

Curr. Genet. 31:15-21(1997).

-I- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate - D-ribose 5-phosphate + D-xylulose 5-phosphate.

-I- COFACTOR: THIAMINE PYROPHOSPHATE.

-I- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                   Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam; pF00456; transketolase; 1.
pfam; pF02779; transket_pyr; 1.
pfam; pF02780; transketolase_C: 1.
TIGRPAMs; TIGR00232; tktlase_bact;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U65983; AABO5935.1; -. HSSP; P23254; 1TRK. InterPro; IPR000360; Transketolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IS-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
Transketolase (EC 2.2.1.1) (TK).
                             SEQUENCE FROM N.A., PHOSPHORYLATION, AN
                                                                                                                                                                                                                                                                                                                                                                          STM2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00801; TRANSKETOLASE_1; PROSITE; PS00802; TRANSKETOLASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97153463; PubMed=9000376;
Jacoby J.J., Heinisch J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase;
                                                                                                        NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASGKGPAVYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2359/152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               679 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                   (Human).
etazoa; Chordata;
theria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thiamine pyrophosphate.
79 AA; 73703 MW; BC5F3
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      646
                                AND
  SEQUENCE OF 15-24, D TISSUE SPECIFICITY and Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42;
                                                                                                                                Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC5F3CF61A78CD4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                        SUBUNIT, GLYCOSYLATION
                                                                                                                                                           Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                          ₹
                                                                                                                                   Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                              Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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RC TISUE=Ovarian carcinoma;
RR Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RR Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Sudo H.,
RN Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RN Nishikawa T., Nagai K., Sugawara M.,
RN Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RN Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RN Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RN Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RN Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RN Watanabe S., Kimura K., Makamura Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Sujawara M.,
RN Watanaba S., Kimura K., John Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nagahari K., Masuho Y.,
RN Yamamoto J., Wakamata Y., Nakamura Y., Nagahari K., Wasuho Y.,
RN Yamamoto J., Wakamata Y.,
RN Yamamata Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21356314; PubMed=11463338; Williams R.T., Manji S.S.M., Parker N.J., Hancock M.S., Walliams R.T., Manji S.S.M., Parker N.J., Hancock M.S., Van Stekelenburg L., Eid J.-P., Senior P.V., Kazenwadel J.S., Shandala T., Saint R., Smith P.J., Dziadek M.A.; "Identification and characterization of the STIM (stromal interaction molecule) gene family: coding for a novel class of transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome Res. 11:422-435(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=2027/1482; PubMed=10819331;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"prediction of the coding sequences of unidentified human
genes. XVII.The complete sequences of 100 new cDNA clones from brain
which code for large proteins in vitro.";
DNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glass.
Ansorge W., Boecher M., Bloecker H., Koehrer S., Blum H.,
Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubne.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mewes H.-W., Otte
Wambutt R., Korn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Amygdala;
MEDLINE=21154917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. use by non-profit institutions as 1
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                                                                       PROSITE; PS50105; SAM_DOMAIN;
Cell adhesion; Transmembrane;
                                                                                                 SMART; SM00454; SAM; PROSITE; PS50105; SA
                                                Phosphorylation.
                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      examined.

pTM: Glycosylated.

pTM: Phosphorylated predominantly

SIMILARITY: CONTAINS 1 SAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Expressed in all tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential)
                                                                                                                                                                      AF328905; AAK82337.1; -.
AB040915; BAA90006.1; ALT_INIT
AL136577; CAB66512.1; ALT_INIT
AK023369; BAB14545.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. 357:673-685(2001).
                                                                                                                                                 IPR001660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293-695 FROM N.A.
  15
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B., Wellenreuther R.,
  14
746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein M., Poustka A.;
                                                                                                                                                 SAM.
       STROMAL
                                                                          1.
Coiled
          INTERACTION MOLECULE
                                                                            coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on
                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                               There
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                                                                                                                                                                                                                                                                                                                                                                     here are no rest
as its content
                                                                            Signal;
                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                               Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor
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                                                                                                                                                                                                                                                                                                                                                                                               restrictions
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ifor
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FAD_binding

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NOS2_CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOS2_CA
054705;
                                                                                                                               WITH MOUSE NOS2).

-!- SUBUNIT: HOMODIMER (BY SIMILARITY).

-!- SUBUNIT: HOMODIMER (BY SIMILARITY).

-!- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG AND COLON. NOT DETECTED IN THE HEART, AORTA, LIVER, KIDNEY, AND SPLEEN.

-!- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS); IN KIDNEY, SPLEEN, AND COLON. EXPRESSION IS REDUCED IN THE PRESENCE OF LPS IN LUNG.

-!- SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                       -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE ENZYME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                              STRAIN-Hartley; TISSUE=Lung;
MEDLINE=98343971; PubMed=9677342;
Shirato M., Sakamoto T., Uchida Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
         EMBL; AF027180; AAC33177.1; HSSP; P29477; 1DD7.
                                                    use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                    -I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESS WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.
-I- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) =
                                                                                                                                                                                                                                                                                                     nitric oxide synthase from gu
Biochem. J. 333:795-799(1998)
                                                                                                                                                                                                                                                                                                                                       GOLO
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cavia porcellus (Guinea
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOS2 OR NOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Inducible NOS) (INOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nitric oxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000
30-MAY-2000
                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          "Molecular cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41
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                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
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W -> WNTRECAAGDSQGPHVHGLVRFDKDFGSYSEYERKH
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Hystricognathi; Caviidae;
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1.14.13.39)
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lung.";
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RESULT REPORT OF THE PROPERTY 
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Best Local
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NS2A_HUMAN STANDARD; PRT; 1153 AA.

P35228; Q16692; O60757; Q16263; O94994;

01-FEB-1994 (Rel. 28, Created)

01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS,
(Inducible NOS) (1NOS) (Hepatocyte NOS) (HEP-NOS).
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Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding; Heme; Multigene family.

Heme; Multigene family.

BINDING 199 199 HEME (BY SIMILARITY).

BOMAIN 508 528 CALMODULIN-BINDING (POTENTIAL).

NP_BIND 622 653 FMN (PYRIMIDINE PART) (BY SIMILARITY).

NP_BIND 766 777 FAD (ADP PART) (BY SIMILARITY).

NP_BIND 902 912 FAD (FLAVIN PART) (BY SIMILARITY).

NP_BIND 907 995 NADP (RIBOSE PART) (BY SIMILARITY).

NP_BIND 1075 1090 NADP (ADP PART) (BY SIMILARITY).

SEQUENCE 1149 AA; 130631 MW; 66D595A2486DB50E CRC64;
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Pfam;
TISSUE-Chondrocytes;
MEDLINE-94068614; PubMed-7504305;
Charles I.G., Palmer R.M.J., Hickery M.S., Bayliss M.T.,
Chubb A.P., Hall V.S., MOSS D.W., Moncada S.;
"Cloning, characterization, and expression of a cDNA encoding inducible nitric oxide synthase from the human chondrocyte.";
Proc. Natl. Acad. Sci. U.S.A. 90:11419-11423(1993).
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-Colorectal adenocarcinoma;
MEDLINE-9403282; PubMed-7693964;
Sherman P.A., Laubach V.E., Reep B.R.,
"Purification and cDNA sequence of an ifrom a human tumor cell line.";
Biochemistry 32:11600-11605(1993).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93234523; PubMed=7682706; Geller D.A., Lowenstein C.J., Shapiro R.A., Nussler A.K., Gellst D.A., Lowenstein C.J., Shapiro R.A., Simmons R.L., Snyder di Silvio M., Wang S.C., Nakayama D.K., Simmons R.L., Snyder Billiar T.R.;
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                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning and expression from human hepatocytes."; Proc. Natl. Acad. Sci. U.S.A. 90:
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erPro; IPR001094; Flavdoxin_like.
erPro; IPR001226; Flavodoxin.
erPro; IPR004030; NO_synthase.
erPro; IPR001433; Oxred_FAD/NAD(P).
m; PF00175; NAD_binding; 1.
m; PF00258; flavodoxin; 1.
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PF02898; NO_synthase; 1.
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57.1%;
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Catarrhini; Hominidae,
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CHARACTERIZATION.
CHARACTERIZATION.
MEDLINE-96047340; PubMed-7558036;
MEDLINE-96047340; PubMed-7558036;
Bloch K.D., Wolfram J.R., Brown D.M., Roberts J.D. Jr., Z
Lepore J.J., Filippov G., Thomas J.E., Jacobh H.J., Bloch
Lepore J.J., Filippov G., Thomas J.E., Jacobh H.J., Bloch
"Three members of the nitric oxide synthase II gene family
"Three members of the nitric oxide synthase II gene family
"Three members of the nitric oxide synthase II gene family
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TISSUE-Airway epithelium;
MEDLINE-95372368; PubMed-7544004;
MEDLINE-95372368; PubMed-7544004;
CHARACTERIZATION.

MEDLINE-9389865; PubMed-9721329;

Taylor B.S., Alarcon L.H., Billie

"Inducible nitric oxide synthase
                                                                                                                                                                                                                                                MEDLINE-95165725; PubMed-7532248; McLay J.S., Chatterjee P., Nicolson Ralston S.H., Grabowski P., Haltes
                                                                                                                                                                                                                                                                                                                                                   Ogawa Y., Nishijima S., Goto M., I "Cloning and characterization of a inducible nitric oxide synthase.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97304504; PubMed-9160867;
MEDLINE-97304504; PubMed-9160867;
Luss H., Li R.-K., ShapIro R.A., Tzeng E.,
Hatakayama K., Geller D.A., Mickle D.A.G.,
Billiar T.R.;
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Erzurum S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and functional expression of human inducible nitric oxide synthase (NOS) cDNA from a glioblastoma cell line A-172.";
J. Biochem. 116:575-581(1994).
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Park C.S., Pardhasaradhi K., Gianotti C., Villegas E., Krishna G.
"Human retina expresses both constitutive and inducible isoforms
nitric oxide synthase mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maier R., Bilbe G., Rediske J., Lotz M.;
"Inducible nitric oxide synthase from human articular chondrocytes:
cDNA cloning and analysis of mRNA expression.";
Biochim. Biophys. Acta 1208:145-150(1994).
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SEQUENCE FROM N.A.
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MEDLINE-94368816; PubMed-7522054;
                                                                                                                                                                                        Hawksworth G.M.; "Nitric oxide production by human proximal tubular immunomodulatory mechanism?"; Kidney Int. 46:1043-1049(1994).
                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Continuous nitric oxide synthesis by inducible n in normal human airway epithelium in vivo."; Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813(1995).
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IL-1, TNF, IFNgamma, and LPS.";
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               PubMed=9721329;
con L.H., Billiar T.R.;
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Simmons
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Li H., Raman C.S., Glaser C.B., Blasko E., Young T.A., F
Whitlow M., Poulos T.L.;
"Crystal structures of zinc-free and -bound heme domain
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MEDLINE=99173237; PubMed=10074942;
Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Li
Dolphin E., Prongay A.J., Reichert P., Lundell D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inducible nitric-oxide synthase. Implications for dimer stability comparison with endothelial nitric-oxide synthase.";
J. Biol. Chem. 274:21276-21284(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biokhimiia 63:766-781(1998)
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                                                                                                                                                                 MIM; 163730;
                                                                                                                                                                                         Genew;
                                            InterPro;
                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weber P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nitric oxide + NADP(+).

COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRE: TERRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OI THE ENZYME (BY SIMILARITY).

ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST WITH MOUSE NOS2). ASPIRIN INHIBITS EXPRESSION AND FUNCTION OF THI ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                   L; AF068236; AAC19133.1
L; AB022318; BAA37123.1
L; S75615; AAD14179.1; A47475; A47475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   produced by alternative splicing.
TISSUE SPECIFICITY: EXPRESSED IN THE LIVER, RETINA,
AIRWAY EPITHELIAL CELLS OF THE LUNG. NOT EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLATELETS.
INDUCTION: BY ENDOTOXINS AND CYTOKINES.
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                                                                                                                                                                                                             2NSI; 07-JAN-00.
4NOS; 04-FEB-00.
                                                                                                                                                                                                                                                            lnsi;
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X73029;
U05810;
U31511;
D26525;
PF00175; NAD_binding;
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                   IPR003097;
IPR001709;
IPR001094;
IPR001226;
IPR001226;
IPR004030;
IPR001433;
                                                                                                                                                                                                                                                            07-JAN-00.
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); AAA36375.1; -.
); CAA51512.1; -.
); AAA56666.1; -.
); AAB49041.1; -.
); BAA05531.1; -.
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                        Oxred_FAD/NAD(P).
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Flavdoxin_like.
                                            NO_synthase
                                                                     Flavodoxin.
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Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Multigene family;
Heme; Phosphorylation; Zinc; Metal-binding; Multigene family;
Alternative splicing; 3D-structure.
BINDING 200 HEME.
BINDING 509 529 CALMODULIN-BINDING (POTENTIAL).
DOMAIN 509 529 CALMODULIN-BINDING PART) (BY SIMILARITY).
NP_BIND 767 778 FAD (ADP PART) (BY SIMILARITY).
NP_BIND 903 913 FAD (FLAVIN PART) (BY SIMILARITY).
NP_BIND 903 913 FAD (FLAVIN PART) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        novel synaptotagmin and a hairless homolog.";
J. Neurosci. 16:7832-7840(1996).
-i- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR
REGULATE ONE OF THE PHASES OF HAIR GROWTH.
-i- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          InterPro; IPR003347;
Pfam; PF02373; jmjC;
                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
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MEDLINE=97141510; PubMed=8987811;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10116;
                                                                                                                                               SEQUENCE
                                                                                                                                                                     Metal-binding
ZN_FING 5
                                                                                                                                                                                                                    Zinc-finger; DNA-binding;
                                                                                                                                                                                                                                                                                        EMBL; U71293; AAC53018.1; ALT_INIT.
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15-JUL-1998 (Rel.
15-JUL-1999 (Rel.
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36, Last sequence update)
38, Last annotation update)
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homolog.";
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01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stoye J.P.;

"Structure and expression of the hairless gene of mice.";

Proc. Natl. Acad. Sci. U.S.A. 91:7717-7721(1994).

-I- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD REGULATE ONE OF THE PHASES OF HAIR GROWTH.

-I- SUBCELLULAR LOCATION: Nuclear.

-I- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN, H FOLLICLES AND INTERFOLLICULAR EPIDERMIS. NO EXPRESSION
_ARATH STANDARD; PRT; 130 AA.

Q92V52;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Expansin-related protein 3 precursor (Ath-ExpGamma-1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metal-binding.
ZN_FING 595
DOMAIN 535
SEQUENCE 1182
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MGD; MGI:96223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Mammalia; Eutheria;
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MEDLINE-94329587;
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Pfam; PF02373; JmjC; 1.
Zinc-finger; DNA-binding; Nuc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: HR MUTATION PRODUCES A NUMBER OF PLEIOTROPIC EFFECTS
INCLUDING STRUCTURAL ABNORMALITIES OF EPITHELIAL CELLS IN THE HAIR
FOLLICLES, HAIR LOSS TOMARDS THE END OF THE FIRST HAIR GROWTH
CYCLE, AND THE FAILURE OF SUBSEQUENT HAIR GROWTH CYCLES. OLDER
MICE CARRYING AN HR MUTATION HAVE BEEN REPORTED TO POSSESS ALTERED
RATIOS OF T-CELL-DEPENDENT B-CELL RESPONSES. MICE HOMOZYGOUS FOR
HR MUTATION ARE UNIQUELY SENSITIVE TO UV AND CHEMICALLY INDUCED
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35, Last sequence update)
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540
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                53.8%;
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                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB Pred. No. 35; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C6-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFBB0EE62AE81B40 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1182
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EXPRESSION IN
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RESULT 13

NOS2_MOUSE STANDARD; PRT; 1144 AA.

AC P29477; O70515; O70516;
DT 01-APR-1993 (Rel. 25, Created)
DT 16-CCT-2001 (Rel. 25, Last sequence update)
DT 16-CCT-2001 (Rel. 40, Last annotation update)
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NC Inducible NOS) (INOS) (Macrophage NOS) (MAC-NOS).

GN NOS2 OR INOSL.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
OX NCBL_TaxID=10090;
RN [1]
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Matches
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; RIKEN Arabidopsis full length cDNA clones (RAFLs) seque SSP consortium (Salk/Stanford/PGEC).", Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases --- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-cv. Columbia;

MEDLINE-20083487; PubMed-10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AC005724; AAD08935.1; ALT_INIT.
EMBL; AY065269; AAL38745.1; -.
PROSITE; PS50842; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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58.3%;
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N-LINKED (GLCMAC. . .) (POTENTIAL).
MISSING (IN REF. 1).
B0C51C6065043BC9 CRC64;
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"The structure of nitric oxide synthase inhibitor complexes.";
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MEDLINE=92357701; PubMed=1379716;
LOWENSTEIN C.J., Glatt C.S., Bredt D.S.,

"Cloned and expressed macrophage nitric c
"Cloned and expressed macrophage nitric c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse macrophages.";
science 256:225-228(1992).
[2]
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MEDLINE=92229444; PubMed=1373522;
Tainer J.A.;
"Structures of the N(omega)-hydroxy-L-arginine complex of inducible "structures of the Nomega) of the North oxide synthase oxygenase dimer with active and inactive
                                                                      MBO J. 10....
[10]
X-RAY CRYSTALLOGRAPHY OF (2.35 ANG)
X-RAY CRYSTALLOGRAPHY OF (2.35 ANG)
Ghosh S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Inducible nitric oxide synthase: role of the N-terminal hook and pterin-binding segment in dimerization and tetrahydrobiopterin interaction."; EMBO J. 18:6260-6270(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS)
MEDLINE=20031637; PubMed=10562538;
Ghosh D.K., Crane B.R., Ghosh S., Wolar
Presta A., Tainer J.A., Getzoff E.D., Serseta A., Serseta
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MEDLLNE-97477482; PubMed-9334294;
Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh
Stuehr D.J., Tainer J.A.;
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J. Biol. Chem.
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                                                                                                                                                              Tainer J.A., Stuehr D.J., Getzoi
"N-terminal domain swapping and
synthase dimerization."
EMBO J. 18:6271-6281(1999).
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"Molecular cloning and functional expression of an oxide synthase from a murine macrophage cell line."
J. Biol. Chem. 267:6370-6374(1992).
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of NF Kappa B in the regulation
ase in an MTAL cell line.",
. Physiol. 269:F718-F729(1995).
                                                                                                                                                                                                                               B.R., Rosenfeld R.J., Arvai A.S., r J.A., Stuehr D.J., Getzoff E.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                  B.R., Arvai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).
                                                                                                                                                                                                                                                                                                                                            279:2121-2126(1998).
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(MAY-1998) to the
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PubMed=9516116;
A.S., Ghosh D.K., W
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Getzoff E.D., Stuehr
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Biochemistry :
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Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).
Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).

-I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.

-I- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
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PIR;
PDB;
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                     PRINTS; PR00369; FLAVODOXIN PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                      MGD;
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MEDLINE=95372392; PubMed=7544010;
                                                                                                                                                                                                                                                                                                                                                       InterPro;
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INDUCTION: BY TREATMENT WITH ENDOTOXINS
SIMILARITY: BELONGS TO THE NOS FAMILY.
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AF065920; AAC17915.1;
AF065921; AAC17916.2;
AF065922; AAC17917.2;
AF065923; AAC17918.2;
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, M92649; -; NOT_ANN
, M84373; AAA39834.1
, U43428; AAC52356.1
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PF00258;
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18-NOV-98.
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23-MAR-99.
23-MAR-99.
23-MAR-99.
08-DEC-99.
04-EEB-00.
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29-MAR-00.
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AAA39834.1; -.
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                                                                             FAD_binding; 1.
NO_synthase; 1.
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STABILIZE T
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Best Local
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NP_BIND
                                                                                                                                                                                                                                       STRAIN-Wistar; TISSUE-Pancreatic islets; MEDLINE-95309542; PubMed-7540573; Karlsen A.E., Andersen H.U., Vissing H., Larse Cuartero B.G., Madsen O.D., Petersen J.S., Mor Mandrup-Poulsen T., Boel E., Nerup J.; "Cloning and expression of cytokine-inducible CDNA from rat islets of Langerhans."; Dlabetes 44:753-758(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning of inducible nitric
muscle cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOS2_RAT STANDARD; PRT; 1147 AA. 206518; P97774; O35765; O35765; Q64558; Q64005; C01-JUN-1994 (Rel. 29, Created)
101-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nitric oxide synthase, inducible (EC 1.14.13.39)
(Inducible NOS) (1NOS).
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CONFLICT
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BINDING
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                   STRAIN-Sprague-Dawley; TISSUE-Astrocytes; MEDLINE-94231594; PubMed-7513765;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-Wistar; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Vascular smooth muscle;
MEDLINE-93191721; PubMed-7680561;
Nunokawa Y., Ishida N., Tanaka S.
                                                                                                              "Cloning and expression astrocytes.";
                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                 MEDLINE-94039059;
                                        TISSUE-Liver;
                                                        SEQUENCE FROM N.A.,
                                                                                                                                               Galea E., Reis D.J.,
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                   PubMed=7693462;
                                                                                             37:406-414(1994).
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                                                      AND
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 Oguchi
                                                                                                                            Feinstein D.L.;
ion of inducible nitric
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oxide synthase in rat
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Sciurognathi;
 Ohshima
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(FLAVIN PART) (BY SIMILARITY).
P (RIBOSE PART) (BY SIMILARITY).
P (ADP PART) (BY SIMILARITY).
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STRAIN SJL/J).
STRAIN BALB/CBYJ).
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Suzuki H.,
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Murinae; Rat
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Michel T., Balligand J.-L.;
"Isolation and characterization of iNOS from rat cardiocytes.";
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOTHER DIVERSE FUNCTIONS THROUGHOUT THE BODY.
-I- CATALYTIC ACTIVITY: L-aginine + N NADPH + M O(2) - citrull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Sprague-Dawley; TISSUE-Hepatocytes;
MEDLINE-93221515; pubmed-7682072;
Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
"Hepatocytes and macrophages express an identical cyto
nitric oxide synthase gene.";
Blochem. Blophys. Res. Commun. 191:767-774(1993).
                                                                                                                                                                                                        SEQUENCE OF 479-655 FROM N.A. STRAIN-Sprague-Dawley; TISSUE-Renal MEDLINE-94276509; PubMed-7516453;
                                                                                                                                                                                                                                                                           STRAIN-Wistar; TISSUE-Renal glomerulus;
Saura M., Zaragoza C., Martinez-Dalmau R.
"Advances in the studies of NO synthesis
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Dahl/Rapp salt sensitive strain MEDLINE-98195092; PubMed-9535415; Chen P.Y., Gladish R.D., Sanders P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning of an inducible nitric polymorphonuclear neutrophils."; Endothelium 2:217-221(1994).
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Tnoue R., Sasayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                calmodulin-dependent nitric-oxide
expression in COS 1 cells.";
Eur. J. Blochem. 217:37-43(1993).
                                                                                                                                                                                                                                                                                                               SEQUENCE OF 509-740 FROM N.A.
                                                                                                                                                                                                                                                                                                                                     salt-sensitive rats.";
Hypertension 31:918-924(1998).
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                                                                                                             TISSUE-Myocardium;
                                                                                                                           SEQUENCE OF 420-479 FROM N.A.
                                                                                                                                                Kidney Int.
                                                                                                                                                                                   Morrissey J.J.,
Klahr S.;
                                                                                                                                                                                                                                                                   cells
                                                                                                                                                                                                                                                                                                                                                   "Vascular smooth muscle nitric salt-sensitive rats.";
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 426-788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Futaki S., Niwa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsutsumishita Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97070590; PubMed-8913516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N
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                                                                                                                                                                                                                                                        Nefrologia 16:35-39(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                     "Advances in cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Sequence analysis of inducible nitric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Molecular cloning of a cDNA encoding
                                                                                                                                                                        Location of
    CAPALYIK COLLEGE (1).

ILLIE OXIGE + N. NADP(+).

COFACTOR: HEME. BINDS ONE MOLE EACH

COFACTOR: HEME. (BH4) WHICH MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                Pharm. Bull. 19:1374-1376(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                             and uterus.";
ENZYME
                                                                                                                                                45:998-1005(1994).
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                                                                                                                                                                                               Kaneto H., Vehaskari M.,
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        OF FAD AND FMN.
STABILIZE THE DI
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         DIMERIC
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                     ALSO REQUIRES
                                          citrulline +
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InterPro;
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EMBL;
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Zinc; Metal-binding; 1
BINDING 197 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00175; NAD_binding; 1. pfam; PF00258; flavodoxin; 1. pfam; PF00667; FAD_binding; 1. pfam; PF02898; NO_synthase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00369; FLAVODOXIN. PRINTS; PR00371; FPNCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004030; NO_synthase.
InterPro; IPR001433; Oxred_FAD/NAD(P).
                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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L; U26686; AAA88861.1; -.
L; U03699; AAC13747.1; -.
L; D12520; BAA02090.1; -.
L; L12562; AAA41720.1; -.
L; X76881; CAA54208.1; -.
L; X76881; BAA07994.1; -.
L; AF006619; AAC16401.1; -.
L; AF006619; AAC16401.1; -.
L; AF006620; AAC16402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: IN NORMAL KIDNEY, EXPRESSED PRIMARILY MEDULLARY THICK ASCENDING LIMB, WITH MINOR AMOUNTS IN THE MEDULLARY COLLECTING DUCT AND VASA RECTA BUNDLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMODIMER (BY SIMILARITY)
TISSUE SPECIFICITY: IN NORMAL KIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY E EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; L36063; AAC02242.1;
JC1472; JC1472.
); P29477; INOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDUCTION: BY INTERFERON GAMMA AND LIPOPOLYSACCHARIDE (LPS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003097; FRD_binding.
IPR001709; FPN_cyt_redctse.
IPR001094; Flavdoxin_like.
IPR001226; Flavodoxin.
IPR004030; NO_synthase.
                                                                                                                                                                                                                                                                                                         197
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PAD (FLAVIN PART) (BY SIMILARITY).

NADP (RIBOSE PART) (BY SIMILARITY).

NADP (ADP PART) (BY SIMILARITY).

ZINC (BY SIMILARITY).

R -> K (IN REF. 7).

R -> Y (IN REF. 3).

C -> R (IN REF. 3).

D -> V (IN REF. 8).

P -> H (IN REF. 8).

P -> G (IN REF. 8).

P -> S (IN REF. 8).

P -> I (IN REF. 3).

D -> E (IN REF. 3).

N -> I (IN REF. 3).

N -> I (IN REF. 3).

N -> P (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                              FAD
FAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEME (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                         (FYKLMIDINE PART) (BY SIMILARITY).

(ADP PART) (BY SIMILARITY).
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ID NSZD_H
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DT 30-MAY
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=Skeletal muscle, and Heart muscle;
MEDITNE=99066690; PubMed=9851365;
Adams V., Krabbes S., Jiang H., Yu J., Ra
Schuler G., Hambrecht R.;
Schuler G., Hambrecht R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
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                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                       EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NS2D_HUMAN STANDARD; PRT; 1147 AA.

060591; 060604;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Nitric oxide synthase, inducible IID (EC 1.14.13.39) (NOS, type II (Inducible NOS) (INOS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nitric Oxide 2:242-249(1998).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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human heart and skeletal muscle of patients with chronic heart
                                                                                                                                                                                                                                                                                                                                                                         -!- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                SIMILARITY).
SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBUNIT: HOMODIMER (BY SIMILARITY).
TISSUE SPECIFICITY: EXPRESSED IN THE H
DURING CHRONIC HEART FAILURE, BUT NOT
SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                          nitric oxide + N NADP(+).
COPACTOR: HEME. BINDS ONE MOLE EACH
TETRAHYDROBIOPTERIN (BH4) WHICH MAY
THE ENZYME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS. MAY BE INVOLVED IN THE PATHOGENESIS OF DILATED CARDIOMYOPATHY OR OF EXERCISE INTOLERANCE OBSERVED IN PATIENTS WITH CHRONIC HEART FAILURE. CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AHGQDPEVFEIPPD
                     AF049656; AAC83553.1;
AF051164; AAC83554.1;
P29477; INOC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heart and skeletal muscle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Human)
                                                                AAC83553.1;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321
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                                                                                                                                                                                                                                                                                        EXPRESSED IN THE HEART AND SKELETAL MUSCLE T FAILURE, BUT NOT IN HEALTHY INDIVIDUALS.
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Pred. No.
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STABILIZE :
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IPR003097; FAD_binding

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Search completed: January 30, 2003, 14:37:56 Job time: 13 secs
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DR InterPro; IPR001226; Flavodoxin_11ke.

DR InterPro; IPR001236; Flavodoxin.

DR InterPro; IPR00130; NO_synthase.

DR InterPro; IPR001433; Oxred_FAD/NAD(P).

DR Pfam; PF00258; flavodoxin; 1.

DR Pfam; PF00258; Flavodoxin; 1.

DR Pfam; PF00258; NAD_binding; Calcium-binding; Calmodulin-binding; MILTS; PR00371; FPNCR.

DR PRINTS; PR00371; FPNCR.

PROSITE: P55001; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding; MILTS; PR00371; FPNCR.

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NADP; FAD; FMN; Calcium-binding; Calmodulin-binding; MILTS; PR00371; PRNCR.

PROSITE: P55001; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding; MILTS; PR00371; PRNCR.

PROSITE: P55001; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding; MILTS; PR0001; NADP; CALMODULIN-BINDING (POTENTIAL).

PR PRINTS; PR00371; FPNCR.

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NADP; CALMODULIN-BINDING (POTENTIAL).

PMN (PYRIMDIDING (POTENTIAL).

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78
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US-08-957-302A-2

US-08-957-302A-2

US-08-14-917-2

US-08-14-917-2

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US-08-14-917-2

US-08-14-917-2

US-08-11-401-2

PCT-US93-11401-2

PCT-US93-11401-2

PCT-US93-11401-2

PCT-US93-77849-2

US-09-287-354-5

US-09-287-354-5

US-09-123-624-2

US-09-123-624-2

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sequence szo, App		•	Sequence 2, A	Sequence 6, A	Sequence 6, A	Sequence 2, A	Sequence 2, A	ุง	Sequence 62,	•	Sequence 62,	Sequence 18,	Sequence 18,	Sequence 4, A	Sequence 2, A	Sequence 192, App	Sequence 7, A	Sequence 2, A
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Best Local Similarity
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ZIP: 77057-2198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,719
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 436
CLASSIFICATION: 436
                                                                                                                                                                                              Sequence 12, Application US/08957302A Patent No. 6046036 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: INT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kelley, Mark R. TITLE OF INVENTION: METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                       APPLICANT: Kelley, Mark
APPLICANT: Williams, David
TITLE OF INVENTION: DNA Sequences Encoding Fusions o
TITLE OF INVENTION: Repair Proteins and Uses Thereof
NUMBER OF SEQUENCES: 16
                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
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                                        CITY: HOUSTON
STATE: TX
                                                                        STREET:
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                                                                        ADDRESSEE: ARNOLD, WH
STREET: P.O. BOX 4433
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                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 78; 100.0%; Pred. No.
                                                                                                                                                     DNA Sequences Encoding Fusions of DNA
                                                                                         WHITE & DURKEE
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Pred. No. 9.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14;
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US-09-336-890-2
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
                                                                                                                                                               TOPOLOGY: 1
37 AAGEGPALYEDPPD 50
                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/957,302A FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                    Match 100.0%;
Local Similarity 100.0%;
                                1 AAGEGPALYEDPPD 14
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                                                                                                                                                                                               amino acid
                                                                      Conservative
                                                                                                                                                               linear
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                                                                        Score 78; DB 3; Pred. No. 2.7e-05;
                                                                                                         Length 318;
                                                                          Indels
                                                                          0,
                                                                          Gaps
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sequence 2, Applic patent No. 6190661 GENERAL INFORMATION: TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: INI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk PRIOR APPLICATION DATA:
APPLICATION NUMBER: SOFTWARE: Patentin Rel CURRENT APPLICATION DATA: NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: TITLE OF INVENTION: FILING DATE: CLASSIFICATION: COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 COUNTRY: USA ZIP: 77057-2198 FILING DATE: APPLICATION NUMBER: HOUSTON Application US/09336890 ; 318 amino acids amino acid TEXAS P.O. Kelley, Mark R.
VENTION: METHODS AND COMPOSITIONS FOR THE USE OF ARNOLD BOX 4433 APURINIC/APYRIMIDINIC WHITE & DURKEE us/09/336,890 US/08/872,719 INDY: 012PZ1

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; STRANDEDNESS: ; TOPOLOGY: 11 US-09-336-890-2
                                                                                  RESULT 6
US-09-668-499-2
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Best Local Similarity luv.
14; Conservative
                              Sequence 2, Application US/09668499
Patent No. 6406917
GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (713) 789-20,
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS: LENGTH: 318 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kelley, Mark
APPLICANT: Williams, David
TITLE OF INVENTION: DNA Sequences Encoding Fusions of DNA
TITLE OF INVENTION: Repair Proteins and Uses Thereof
APPLICANT: Kelley, Mark R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE USE OF APURINIC/APYRIMIDINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: INDY:005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                 Watch 100.0%; Local Similarity 100.0%; local Similarity 100.0%; los 14; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: HOUSTON
STATE: TX
                                                                                                                                                   37 AAGEGPALYEDPPD 50
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STREET: P.O. BOX 4433
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Pred. No. 2.7e-05;
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Pred. No. 2.7e-05;
Mismatches 0;
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Query Match
Best Local Similarity
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Patent No. 598607
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ZIP: 77057-21>
COMPUTER READABLE FORM:
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TAMPUTER: PC-DOS/MS-DOS
TAMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 2:
                         SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,
FILING DATE:
                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                      APPLICANT: HANDA, HIROSHI
APPLICANT: KAWAGUCHI, Haruma
TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND
TITLE OF INVENTION: PROCESS OF PURIFYING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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ADDRESSEE: ARNOLD, WI
PRIOR APPLICATION DATA:
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                                                                               COMPUTER: IBM COMPUTER: OPERATING SYSTEM:
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                                                                                                                                                                                CITY: Boston
STATE: MA
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CLASSIFICATION:
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            CLASSIFICATION: 435
                                                                                                                                                     ZIP: 02109
                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acids
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О.
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                                                                                       IBM Compatible SYSTEM: DOS
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                                                                                                                     Diskette
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                                            US/08/795,927
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Pred. No. 2.7e-05;
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ATTORNEY/AGENT INFORMATION: NAME: Corless, Peter F

NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860

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US-08-957-302A-2
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Best Local Similarity
Matches 14; Conserv
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Best Local Similarity
                            Query Match
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: INDY
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
                                                                                                                                                          TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,302A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DNA Sequences Encoding rusions of TITLE OF INVENTION: Repair Proteins and Uses Thereof NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                             STRANDEDNESS:
TOPOLOGY: li
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                     FILING DATE: Concurrently Herewith CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 77210-4433
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                                                                                                                          LENGTH:
                                                                                                             amino acid
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                                                                                                                          524 amino acids
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                                                                             linear
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             100.0%;
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Pred. No.
             Score
Pred.
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             78;
             DB 3;
. 4.6e-05;
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US-09-126-109-12
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US-09-542-403-2
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                                                        GENERAL INFORMATION:
APPLICANT: Thigpen
APPLICANT: Hohmeie
APPLICANT: Newgard
APPLICANT: Unger,
                                                                                                                                   Sequence 12, Application US/09126109 Patent No. 6171856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
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Best Local Similarity
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                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: INI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE STREET: P.O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kelley, Mark
APPLICANT: Williams, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
 APPLICANT:
                 APPLICANT:
                                                                                                                                                                                                                            243 AAGEGPALYEDPPD 256
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                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/542,403
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                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                          Thigpen, Anice
Hohmeier, Hans Ewald
Newgard, Christopher B
Unger, Roger H.
Shimabukuro, Michio
Chen, Guaxun
                                                                                                                                                                                                                                                                                                                                                                                                           524 amino acids
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Hugl, Sigrun R.
               Rhodes,
                                                                                                                                                                                                                                                                                                                                                              linear
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713) 789-2679
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               Christopher J.
                                                                                                                                                                                                                                                                                   100.0%; Score 78; 100.0%; Pred. No. tive 0; Mismatch
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Best Local
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                                                                                                                                                                                                                                                                                                                               Patent No. 5468630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,092
FILING DATE: 30-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US Unknown
FILING DATE: 03-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: MCM1111an, Nabeela R.
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (512) 474-7577 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                             APPLICANT: Billiar, Timothy R.
APPLICANT: Nussler, Andreas K.
APPLICANT: Geller, David A.
APPLICANT: Simmons, Richard L.
TITLE OF INVENTION: CDNA Clone for Human Inducible Nitric
TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cousin, TITLE OF INVENTION:
                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (512) 418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                           311 ANGROPELFEIPPD 324
                                   COUNTRY: U
ZIP: 15219
                                                                       STREET: 600 Grant
CITY: Pittsburgh
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MCMIllian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSD:560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/126,109 FILING DATE: 30-JUL-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: P.O. I
                                                                                                        ADDRESSEE: Arnold B. Silverman
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 600 Grant Street, 42nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 8; Conserv
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VENTION: METHODS AND COMPOSITIONS RELATING
VENTION: TO NO-MEDIATED CYTOTOXICITY
EQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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RESULT 12
US-08-265-046-2
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SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/265,046
FILING DATE: 24-JN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Gould, Lewis F. Jr.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 119130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
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TELEX: 866172
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 566-6000
TELEPAX: (412) 566-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION UDATE: US/07/981,344
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,917
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Richard L. Simmons
TITLE OF INVENTION: Inducible Nitric Oxide Synthase
TITLE OF INVENTION: Gene for Treatment of Disease
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Bolo----
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 19103
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market Street, Suite 3232
                                                                                                                                                                                                                                                                                                                                        STREET: 1700 Market CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Silverman, Arnold REGISTRATION NUMBER: 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAGEGPALYEDPPD 14
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es θ; Conserva
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David A. Geller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Timothy R. Billiar
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57.1%;
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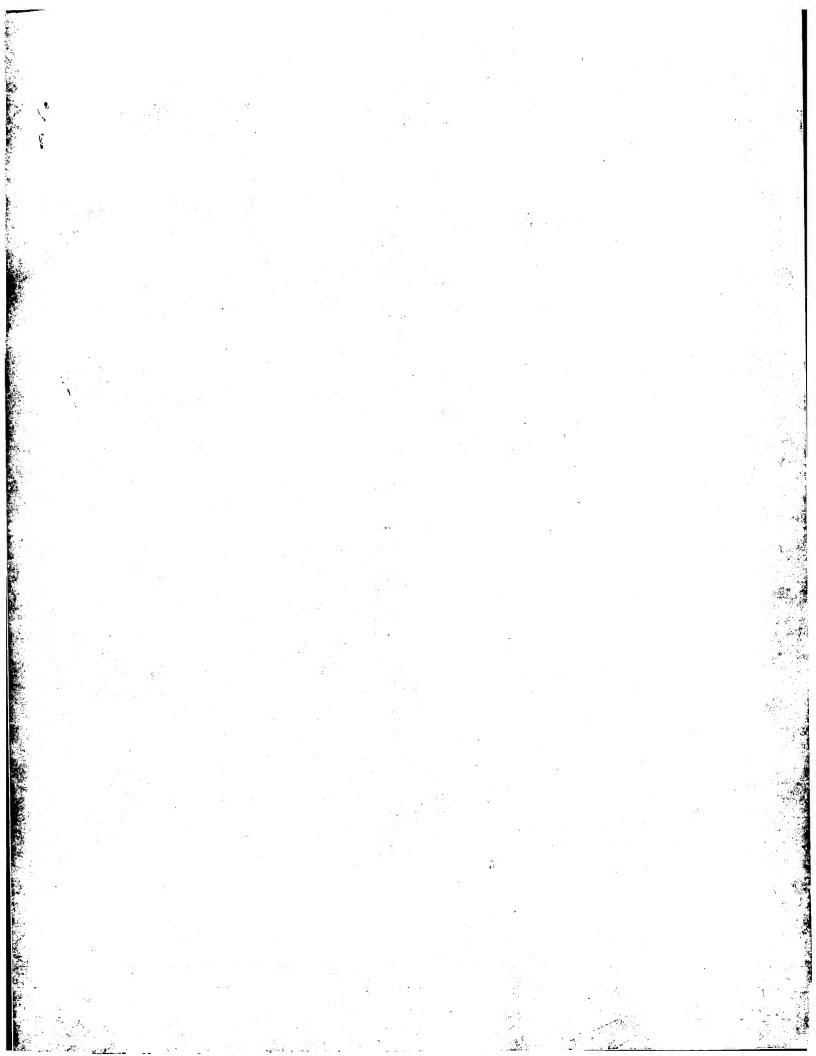
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                                                                                                                             Query Match
Best Local Similarity
Whes 8; Conserve
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RESULT 14
PCT-US93-11401-2
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Best Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOULD, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 116972-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6020
TELEFAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Simmons, Richard L.

TITLE OF INVENTION: CDNA Clone for Human Inducible Nitric
TITLE OF INVENTION: Oxide Synthase And Process for Preparing Same
                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                             311 ANGRDPELFEIPPD 324
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nes 8; Conservative
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CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 1700 Market St. Suite 3232
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Nussler, Andreas K.
Geller, David A.
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57.1%;
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Pred. No.
                                                                                                                                                            Score 42; DB Pred. No. 80;
                                                                                                                                              Mismatches
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80;
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PCT-US95-07849-2
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                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9507849
GENERAL INFORMATION:
APPLICANT: University of Pittsburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PCTUS9311401 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Arnold B.
REGISTRATION NUMBER: 22,614
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lewis F. Gould, Jr.
ADDRESSEE: Eckert Seamans Cherin & Mellott
ADDRESSEE: 1700 Market Street, Suite 3232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino aci
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APPLICATION NUMBER: US/07/981,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                     TITLE OF INVENTION: Inducible Nitric Oxide Synthase TITLE OF INVENTION: Gene for Treatment of Disease
                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                               311 ANGRDPELFEIPPD 324
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ADDRESSEE: Eckert Seamans Cherin & Mellott
STREET: 600 Grant Street, 42nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 86617
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                                   ZIP: 19103
                                                                                       CITY:
                                                                                                                                                                                                                                                                                                                                                                                             1 AAGEGPALYEDPPD 14
                                                   COUNTRY:
                                                                     STATE:
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                                                                                     Philadelphia
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NVENTION: cDNA Clone for
NVENTION: Oxide Synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: (412) 566-6000
(412) 566-6099
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Geller, David A.
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                                                       USA
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                                                                                                                                                                                                                                         University of Pittsburgh of the Commonwealth System of Higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Pred. No.
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And Process for Preparing Same
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
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0;

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION LATA:
APPLICATION NUMBER: PCT/US95/07849
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: PCT/US95/07849
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: PCT/US95/07849
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: 119130-2
REFERENCE/DOCKET NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 21,010-2
REFERENCE/DOCKET NUMBER: 21,010-2
REFERENCE/DOCKET NUMBER: 21,010-2
REFERENCE/DOCKET NUMBER: 25,057
REFER
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                    : /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_REW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_REW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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1: /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compugen
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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10 US-09-992-056-2
US-09-870-759-124
US-09-870-759-124
US-09-925-36041
10 US-09-925-300-1432
US-09-9738-626-6643
3 US-09-994-365-2
10 US-09-994-365-2
10 US-09-994-365-2
10 US-09-915-242-11073
10 US-09-815-242-11073
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US-10-003-014-2

US-10-001-426-4

US-10-003-014-4

0 US-09-925-300-1188

0 US-09-925-397-551
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Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 551, Appli
Sequence 552, Appli
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Sequence 3, Appli
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US-10-001-426-2
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KAWAGUCHI, Har
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Sequence 3, Appli	US-09-922-378-3	10	204		36	
Sequence 42871, A) US-09-864-761-42871	10	88	46.2	36	
Sequence 240, App	US-09-981-87	ø	71	٠	36	
239	us-	ø	71	46.2	36	
Sequence 4, Appli	US-10-034	ø	3472	٠	37	
4, App	us-	9	3472	47.4	37	
104,	US-1(12	750	47.4	37	
e 944,	US-09-822-	10	750	47.4	37	
104,	US-10-	ø	750	47.4	37	
104,	us-10-	9	750	47.4	37	
104,	US-10-174-590-	ø	750	47.4	37	
618,	us-09-	ø	750	47.4	37	
618,	US-09-999-832A-618	9	750	47.4	37	
944,	us-09-895-	ø	750	47.4	37	
Sequence 618, App	US-09-978	ø	750	47.4	37	
618,	US-09-978-697-6	ø	750	47.4	37	
618,	US-09-978	o	750	47.4	37	
42	US-09-	10	733	47.4	37	
Sequence 7, Appl1	-60 - Sn	10	448	47.4	37	
43251	·60-sn	10	378	47.4	37	
e 888,	US-09-925-	10	368	47.4	37	
e 192, A	US-09-879-957-	10	355	47.4	37	
e 1) US-09-925-301-1078	10	171	47.4	37	
Sequence 4, Appli	US-09-942-117-4	v	91	47.4	37	
Sequence 14, Appl	US-09-942-117-14	ø	15	47.4	37	
Sequence 11759, A	US-09-815-242-11759	10	458	48.7	38	

ALIGNMENTS

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TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
                                                                                          PRIOR APPLICATION DATA:
APPLICATION UNMBER: 09/440,597
PILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: COrless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 47115
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/001,426
FILING DATE: 02-NO. US20020160472A1-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE Dike, Bronstei
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND PROCESS OF PURIFYING PROTEINS
                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
COUNTRY: USA
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bronstein, Roberts & Cushman, LLP
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal

TOPOLOGY: linear MOLECULE TYPE: peptid

peptide

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US-10-003-014-2
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                                           SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-10-003-014-2
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Best Local
Query Match
Best Local Similarity
                                                                                                                                                                                                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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les 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/440,597
FILING DATE: 15-No. US20020169293A1-1999
APPLICATION NUMBER: 08/795,927
FILING DATE: <Unknown>
ATTORNEY/AGENT_INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAWAGUCHI, Haruma TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/003,014
ETILING DATE: 02-No. US20020169293A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HANDA, Hiroshi
                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                     ORIGINAL
                                                                                                                      HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                    FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                    NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 47115
                                                                                                                                                                                                                              LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                   TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                         SOURCE:
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   100.0%;
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   Score 78; DB 9;
Pred. No. 2.2e-06;
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                    Length 14;
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US-10-001-426-4
                                                            RESULT 4
US-10-003-014-4
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            Sequence 4, Application US/10003014 Patent No. US20020169293A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   37
                                                                                                                                                                                                               Match 100.0%;
Local Similarity 100.0%;
                                                                                                                               1 AAGEGPALYEDPPD 14
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37 AAGEGPALYEDPPD 50
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COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND PROCESS OF PURIFYING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: COIless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 471
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/440,597
ETILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: COIless, Peter F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 4:
APPLICANT: HANDA, Hiroshi
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STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 319 amino acids TYPE: amino acid
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Pred. No. 5.8e-05;
); Mismatches 0;
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US-09-925-300-1188
Sequence 1188, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEO ID NOS: 1890
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                             APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 15-NO. US20020169293A1-1999
APPLICATION NUMBER: 08/795,927
FILING DATE: <UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: COrless, Peter F
REGISTRATION NUMBER: 33,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/003,014
FILING DATE: 02-No. US20020169293A1-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-6440
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MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESSE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
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                                                                                                                                                                                                                                                                                                                                                                                                       AAGEGPALYEDPPD 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 319 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 319;
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US-09-992-056-2
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                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09992056 Patent No. US20020061862A1 GENERAL INFORMATION:
               APPLICANT: Billiar, Timothy R.
APPLICANT: Tzeng, Edith
APPLICANT: Nussler, Andreas K.
APPLICANT: Geller, David A.
APPLICANT: Simmons, Richard K.
APPLICANT: Shears II, Larry L.
TITLE OF INVENTION: Inducible Nitric Oxide Synthase Gene for Treatment of
TITLE OF INVENTION: Disease
FILE REFERENCE: 213298
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/176,496
PRIOR FILING DATE: 1998-10-21
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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (46)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids us-o9-925-300-1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-925-297-551
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 551
LENGTH: 68
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 551, Application US/09925297 Patent No. US20020081659A1 GENERAL INFORMATION:
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Matches
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LENGTH:
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Matches
                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: SITE
LOCATION: (175)
                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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39
                                                               Local Similarity 61.9 es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity es 14; Conserv
                             1 AAGEGPALYEDPP 13
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AAGQEPCXLEDPP 51
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                                                                              56.4%;
                                                               Score 44; DB 1
Pred. No. 1.9;
1; Mismatches
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1995-06-05

08/314,917

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US-09-870-759-124

; Sequence 124, Application US/09870759

; Patent No. US20020177551A1
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LENGTH: 1153
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Best Local
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PRIOR FILING DATE: 1992-11-25
NUMBER OF SEQ ID NOS: 2
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PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1994-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TERMAN, DAVID S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 ANGRDPELFEIPPD 324
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les 8; Conserv
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                      NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
STREET: Two Embarcadero Center,
                                                                                                                                                                                                          TITLE OF
                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1144
                                                    COUNTRY: USA
                                                                   CITY: San Francisco
STATE: California
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Maylie, James
Bond, Chris T.
Silvia, Christopher P.
Silvia, Christopher P.
INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
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57.1%;
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Pred. No. 1e+0
3; Mismatches
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Pred. No.
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73;
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1e+02;
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Best Local Similarity
""" hes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-254-590-1
                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09254590 Patent No. US20020165379A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 GSGPGALGRDPPD 45
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FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
                                   ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                       NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE Two Embarcadero Center, Eighth Floor
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                     Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels
                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Protein
LOCATION: 1.561
OTHER INFORMATION: /note= "human st
calcium-activated potassium channel
protein 1 (hSK1)"
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                                                                                                                 CITY: San Francisco
STATE: California
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                                                                                                COUNTRY: USA
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Maylie, James
Bond, Chris T.
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Pred. No. 84;
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-254-590-1
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US-10-115-695-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                 COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: WO PCT/US97/16033 FILING DATE: 10-SEP-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Adelman, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/026,451 FILING DATE: 11-SEP-1396 APPLICATION NUMBER: US 60/040,052 FILING DATE: 07-MR-1997 APPLICATION NUMBER: US 60/045,233 FILING DATE: 17-APR-1997 FILING DATE: 17-APR-1997
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protein 1 (hSK1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..561
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
     APPLICATION NUMBER: US/10/115,695
                                                                                                                                      COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                         STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 10-Mar-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 561 amino acids
                                                                                                                                                                                                                                                                                                                            Silvia, Christopher P. INVENTION: Small and Intermediate Conductance,
                                                                                                                                                                                                                                                                                                                                                                 Maylie, James
Bond, Chris T.
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1..561
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                                                                                                                                                                                                                                                                                       Calcium-Activated Potassium Channels and Uses Thereof
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Pred. No. 84;
O; Mismatches
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                                            Version #1.30
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ORGANISM: HOMO SAP16
FEATURE:
NAME/KEY: SITE
LOCATION: (114)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (193)
OTHER INFORMATION: X
                                                                                                                                                          TYPE: PRT
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sapiens

Xaa equals any

of the naturally occurring L-amino acids

Xaa equals any of the

naturally occurring L-amino acids

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RESULT 12
US-09-925-300-1432
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NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1432
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                              Sequence 1432, Application US/09925300 Patent No. US20020151681A1
                                                            CURRENT APPLICATION NUMBER: US/09/925,300 CURRENT FILING DATE: 2001-08-10 PRIOR APPLICATION NUMBER: CT/US00/05988 PRIOR FILING DATE: 2000-03-08 PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                    APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
                                                                                                                                                                                                                                   APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                          33 GSGPGALGRDPPD 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GEGP-ALYEDPPD 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: /note= "human scalcium-activated potassium channel protein 1 (hSK1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/254,590 FILING DATE: 10-Mar-1999 APPLICATION NUMBER: US 60/026,451 FILING DATE: 11-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein 
LOCATION: 1..561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION DATA:
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Pred. No. 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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; NAME/KEY: SITE ; LOCATION: (201) ; OTHER INFORMATION: US-09-925-300-1432

Xaa equals any of the naturally occurring L-amino acids

Query Match
Best Local Similarity
Matches 8; Conserv

Conservative

0; Mismatches

50.0%; 72.7%;

Score 39; DB Pred. No. 34;

10; ω ••

Length 201;

Indels

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Gaps

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70 GEEEALKEDPP 80

3 GEGPALYEDPP 13

Sequence 6643, Application US/09738626 Publication No. US20020197605A1

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HIROSHI

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                                                                                                                                                                                                                                                                                                                  RESULT 14
US-10-077-130-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
SEQ ID NO 6643
LENGTH: 563
TYPE: PRT
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    Sequence 5, Application US/10077130 Patent No. US20020168742A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 5
                                                          APPLICANT: Acton, Susan L.

TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
TITLE OF INVENTION: Members and Uses Therefor
FILE REFERENCE: MPI2001-047P1RCP1(M)
CURRENT APPLICATION NUMBER: US/10/077,130
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/269201
PRIOR FILING DATE: 2001-02-15
                                                                                                                                                                                                              APPLICANT: Kapeller-Libermann, Rosana APPLICANT: Acton, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT: OZAKI, AKIO
LITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
LE REFERENCE: 249-125
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les 8; Conserv
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                       FastSEQ for Windows Version 4.0
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TATEISHI, NAOKO
SENOH, AKIHIRO
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nilarity 53.3%;
Conservative
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, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 9; Pred. No. 1e+02; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
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                                                                                                            Query Match
Best Local Similarity
"hehes 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-09-994-365-3
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Search completed: January 30, 2003, 14:42:23 Job time: 11 secs
                                                                                                                                                                                        US-09-994-365-3
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                                                                                                                                                                                                                                                     SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09994365 Patent No. US20020115148A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/253,592
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/256,839
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: McEuen, Mark TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis FILE REFERENCE: CECHI18109
CURRENT APPLICATION NUMBER: US/09/994,365
CURRENT FILING DATE: 2001-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Charmley, Patrick
                                                                                                                                                                                                     LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 7968
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Local Similarity 57.1%;
es 8; Conservation
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                                                                                            6 PALYEDPP 13
                                                                PPLFEDPP 43
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                                                                                                                             Conservative
                                                                                                                                            48.7%;
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    Mismatches

                                                                                                                                             Score 38; DI
Pred. No. 27;
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Pred. No. 1.6e+03;
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                                                                                                                                                          DB 10;
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Minimum DB
Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/1/paa/US083_COMB.pep:
/cgn2_6/ptodata/1/paa/US083_COMB.pep:
/cgn2_6/ptodata/1/paa/US085_COMB.pep:
/cgn2_6/ptodata/1/paa/US085_COMB.pep:
/cgn2_6/ptodata/1/paa/US085_COMB.pep:
/cgn2_6/ptodata/1/paa/US085_COMB.pep:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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  US-10-001-426-2

US-10-003-014-2

US-10-003-014-2

US-10-029-386-28638

US-09-834-366-16628
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(without alignments)
64.937 Million cell updates/sec
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	23	21	21	21	21	21	21	21	L	23	_	22	24	24	18	27	27	26	23	21	21	21	21	21	19	13	21	27	-	22	21	26	25	21	21	26	-	21
-09-791-	0	-09-791-537-	-09-791-537-1	-791-537-4	-09-791-537-6777	-09-791-537-1	-09-791-537-	37-	08-957-302-	-09-925-300-1	T-US00-05988,-11	-09-805-020-4	-10-003-014-4	-001-426-4	4	-60-323-784-1	S-60-240-409-938	S-10-247-671-	-09-976-5	-09-791-537-1	-09-791-537-79508	-09-791-537-7	-09-791-537-	S-09-791-537-3	-09-522-04	S-08-957-302-	S-09-791-537-	S-60-324	T-US02-30474-172	S-09-805-020-48	-09-791-5	S-10-216-436-	S-10-153-088-7	S-09-760-485-8	S-09-760-482-73	-10-264-049-408	T-US01-18569-4	US-09-791-537-41381
145	Sequence 12583, A	6771	equence 114	ø	e 67773	equence 130991	e 8668,	e 91767	O	e 1188,	1188,	e 49,	equence 4,	e 4,	e 4,		936	e 131,	e 938, A	e 11457	O	ው	61013	318	2, A	e 12, A	e 125777	e 1730,	1725,	equence 48, A	e 1022	Sequence 815, App	e 73,	e 815,	e 73, Ap	e 4083,	quence 4083, Ap	Sequence 41381, A

ALIGNMENTS

RESULT 1

US-09-440-597-2

IS-09-440-597-2

Sequence 2, Application US/09440597

GENERAL INFORMATION:
APPLICANT: HANDA, Hiroshi
KAWAGICHI, Haruma

TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A
PROCESS OF PURIFYING PROTEINS

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION NUMBER: US/09/440,597
FILING DATE: 15-NOV-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/795,927

PRIOR APPLICATION NUMBER: 08/795,927

ATTORNEY/AGENT INFORMATION:

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RESULT 2
US-10-001-426-2
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GENERAL INFORMATION:
APPLICANT: HANDA, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                       TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION NUMBER: US/10/001,426
FILING DATE: 02-NOV-2001
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAGEGPALYEDPPD 14
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: COTLESS, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 47115
TELEPHONE: 617-523-3400
        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A PROCESS OF PURIFYING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 47115
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                       TYPE: amino acid
                                     STRANDEDNESS: single
                                                                       LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/440,597 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: MA
                                                                                                                                           TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 617-523-34 TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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Pred. No. 2.
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2.7e-05;
les 0;
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US-10-003-014-2
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      Matches
                                 Query Match
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                          STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 2
                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/440,597
FILING DATE: 15-Nov-1999
APPLICATION NUMBER: 08/795,927
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/003,014
FILING DATE: 02-Nov-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A PROCESS OF PURIFYING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HANDA, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
                  Similarity
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14; Conservative
                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
                                                                                                                                                                                                                   LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                             TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                         NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP STREET: 130 Water Street
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                 Score 78; Pred. No.
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Pred. No. 2
 Mismatches
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                 2.7e-05;
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                             Length 14;
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1 AAGEGPALYEDPPD 14

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Query Match
Best Local Similarity
"hese 14; Conserve
                                                                                                    ; OTHER INFORMATION: Xaa - Pro, Thr US-09-834-366-16628
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US-09-834-366-16628
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                                                                                                                                                                                                                                                 SOFTWARE: Patent.pm
SEQ ID NO 16628
LENGTH: 73
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Best Local :
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 28638
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28638, Application US/10029386
                                                                                                                                                                                                                                                                                                            APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.052.REG
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/197,873
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwards,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: MAP TO CHR14.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2

OTHER INFORMATION: SWISSPROT HIT: P27695, EVALUE 3.00e-24
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                                                                                                                                            NAME/KEY: UNSURE LOCATION: 59
                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                    TYPE: PRT
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                 100.0%;
ilarity 100.0%;
Conservative 0
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IN ADULT LIVER, SIGNAL = 0.91
IN PLACENTA, SIGNAL = 1.6
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                 Score 78; DB 22;
Pred. No. 0.00018;
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Pred. No.
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                   Gaps
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LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: UNSURE
; LOCATION: 59
; OTHER INFORMATION: Xaa - Pro,Thr
US-60-197-873-16628
PCT-US01-18569-4083; Sequence 4083, Application PC/TUS0118569; GENERAL INFORMATION:
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US-09-791-537-41381
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US-60-197-873-16628
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Matches
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 133055
SOFTWARE: PatentIn version 3.0
SEO ID NO 41381
LENGTH: 146
TYPE: PRT
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SOFTWARE: Patent.pm
SEQ ID NO 16628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16628, Application US/60197873 GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2000-04-18
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APPLICANT: Giordano, Jean-Y
TITLE OF INVENTION: ESTS ar
FILE REFERENCE: 81.US1.PRO
                                                                                           37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 AAGEGPALYEDPPD 501
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nes 14; Conserv
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Pred. No.
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Pred. No.
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RESULT 10
US-09-760-482-73
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            Sequence 73, Application US/09760482
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, a
FILE REFERENCE: PTZ60
CURRENT APPLICATION NUMBER: US/09/760,482
CURRENT FILING DATE: 2001-01-16
Prior application data removed - consult PALM
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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SEQ ID NO 4083
LENGTH: 170
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SEQ ID NO 4083
LENGTH: 170
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Best Local
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CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Birse et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA133P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA133PCT
CURRENT APPLICATION NUMBER: PCT/US01/18569
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,467
PRIOR FILING DATE: 2000-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-06
NUMBER OF SEQ ID NOS: 4360
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                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (61)
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (61)
OTHER INFORMATION: Xaa
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Pred. No.
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Pred. No.
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J.00049;
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            file wrapper
                                                                                  Antibodies
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US-10-153-088-73
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              SOFTWARE: PATENTIN VER.
SEQ ID NO 73
LENGTH: 183
TYPE: PRT
                                                                                                                                                                Sequence 73, Application US/10153088
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                FILE REFERENCE: PTZ60C1N
CURRENT APPLICATION NUMBER: US/10/153,088
CURRENT FILING DATE: 2002-05-23
                                                                             Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 215
ORGANISM:
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Homo sapiens

and Antibodies

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; OTHER INFORMATION: US-09-760-485-815
                                                                                                                                                                                                                                                                                                                                                                                          US-09-760-485-815; Sequence 815; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-760-482-73
                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 815
LENGTH: 183
TYPE: PRT
                                                             Query Match
Best Local Similarity
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TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/760,485
CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                 Prior application data removed - NUMBER OF SEQ ID NOS: 1477
                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PJZ17
                                                                                                                               NAME/KEY: SITE LOCATION: (182)
                                                                                                                                                          LOCATION: (175)
OTHER INFORMATION:
                                                                                                                                                                                                 ORGANISM: Homo sapiens FEATURE:
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NAME/KEY: SITE
LOCATION: (182)
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LOCATION: (175)
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US-10-216-436-815
Sequence 815, Application US/10216436
GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/760, 485
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179, 065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/214, 886
PRIOR TILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214, 886
PRIOR APPLICATION NUMBER: 60/217, 487
PRIOR FILING DATE: 2000-07-11
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/225, 758
PRIOR APPLICATION NUMBER: 60/220, 963
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220, 963
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
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Best Local :
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                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Homo saplens FEATURE:
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LOCATION: (182)
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LOCATION: (175)
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LOCATION: (182)
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LOCATION: (175)
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OR FILING DATE: 2000-07-11
OR APPLICATION NUMBER: 60/225,447
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/218,290
OR FILING DATE: 2000-07-14
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Sequence 48, Application US/09805020
GENERAL INFORMATION:
APPLICANT: LEVINE, ZURİt
TITLE OF INVERTION: SPLICE VARIANTS OF ONCOGENES
FILE REFERENCE: 2786-0168P
CURRENT APPLICATION NUMBER: US/09/805,020
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 48
LENGTH: 295
TYPE: PRT
Search completed: January 30, 2003, 14:41:41 Job time: 141 secs
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US-09-805-020-48
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US-09-791-537-102207
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SOFTWARE: Patentin version 3.0
SEQ ID NO 102207
LENGTH: 287
TYPE: PRT
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GENERAL INFORMATION:
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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| Cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
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Query Match 100.0%; Score 78; DB 5; Length 282; Best Local Similarity 100.0%; Pred. No. 1.6e-05; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 2 US-09-724-676-91739, Application US/09724676 Sequence 91739, Application US/09724676 GENERAL INFORMATION: APPLICANT: Compugen LTD FILLE REFERENCE: 129181.4 Compugen of alternative splicing FILLE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SOFTWARE: PAT TYPE: PRT ORGANISM: Homo sapiens US-09-724-676-91739	Query Match Query Match 100.0%; Score 78; DB 5; Length 282; Best Local Similarity 100.0%; Pred. No. 1.6e-05; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AAGEGPALYEDPPD 14	RESULT 1 US-09-724-676-91737, Application US/09724676 Sequence 91737, Application US/09724676 GENERAL INFORMATION: APPLICANT: Compugen LTD FILE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION UNMEER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: PatentIn version 3.2 SEQ ID NO 91737 LENGTH: 282 TYPE: PRT ORGANISM: Homo sapiens US-09-724-676-91737	ALIGNMENTS	27 78 100.0 295 5 US-09-724-676A-91755 Sequence 91755, A 28 78 100.0 298 5 US-09-724-676A-91730 Sequence 91760, A 29 78 100.0 298 5 US-09-724-676-91733 Sequence 91733, A 30 78 100.0 298 5 US-09-724-676A-91734 Sequence 91733, A 31 78 100.0 298 5 US-09-724-676A-91734 Sequence 91733, A 32 78 100.0 305 5 US-09-724-676A-91735 Sequence 91733, A 33 78 100.0 305 5 US-09-724-676A-91735 Sequence 91735, A 36 78 100.0 305 5 US-09-724-676A-91736 Sequence 91735, A 37 78 100.0 316 5 US-09-724-676A-91736 Sequence 91735, A 38 78 100.0 316 5 US-09-724-676-91744 Sequence 91735, A 39 78 100.0 316 5 US-09-724-676-91744 Sequence 91744, A 39 78 100.0 316 5 US-09-724-676-91756 Sequence 91744, A 40 78 100.0 316 5 US-09-724-676-91768 Sequence 91767, A 41 78 100.0 316 5 US-09-724-676-91768 Sequence 91767, A 42 78 100.0 316 5 US-09-724-676-91768 Sequence 91767, A 43 78 100.0 316 5 US-09-724-676-91768 Sequence 91767, A 44 78 100.0 316 5 US-09-724-676-91744 Sequence 91767, A 47 78 100.0 316 5 US-09-724-676-91744 Sequence 91767, A 48 78 100.0 316 5 US-09-724-676-91744 Sequence 91767, A 49 78 100.0 316 5 US-09-724-676-91744 Sequence 91767, A 40 78 100.0 316 5 US-09-724-676-91768 Sequence 91767, A 41 78 100.0 316 5 US-09-724-676-91744 Sequence 91767, A 42 78 100.0 316 5 US-09-724-676-91744 Sequence 91767, A 43 78 100.0 316 5 US-09-724-676-91744 Sequence 91767, A 44 78 100.0 316 5 US-09-724-676A-91744 Sequence 91767, A 45 78 100.0 316 5 US-09-724-676A-91744 Sequence 91767, A 46 78 100.0 316 5 US-09-724-676A-91744 Sequence 91765, A

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RESULT 3
US-09-724-676A-91737
US-09-724-676A-91737
Sequence 91737, Application US/09724676A
SEQUENCE INFORMATION:
APPLICANT: Compugen LTD
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129.181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTAL VERSION 3.2
LENGTH: 282
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-91737
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US-09-724-676A-91739
US-09-724-676A
Sequence 91739, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
APPLICANT: Compugen LTD
TILE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 91739
LENGTH: 282
TYPE: PRT
CORANISM: Homo Sapiens
US-09-724-676A-91739
                                                                                Sequence 91745, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 91745

LENGTH: 293
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US-09-724-676-91745
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US-09-724-676-91745
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Pred. No. 1.6e-05;
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Pred. No. 1.6e-05;
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FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 91746
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676-91746
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 91758
LENGTH: 293
TYPE: PRT
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US-09-724-676-91746
                               Sequence 91759, Application US/09724676

GENERAL INFORMATION:
APPLICANT: Compugen LTD
TIPLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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US-09-724-676-91758
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US-09-724-676-91759
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
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SEQ ID NO 91759
LENGTH: 293
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Pred. No. 1.7e-05;
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RESULT 10
US-09-724-676-91770
Sequence 91770, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTMARE: PatentIn version 3.2
SEQ ID NO 91770
LENGTH: 293
RESULT 11
US-09-724-676A-91745
; Sequence 91745, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
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US-09-724-676-91770
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US-09-724-676-91769
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
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Best Local Similarity
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SOFTWARE: Patentin version 3.2
SEQ ID NO 91769
LENGTH: 293
TYPE: PRT
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 91745
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-91745
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APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676A

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 91746

SEQ ID NO 91746

SEQ ID NO 91746
RESULT 14.
US-09-724-676A-91759
· Sequence 91759, Application US/09724676A
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US-09-724-676A-91746
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US-09-724-676A-91758
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                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/724,676A CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SEQ ID NO 91758 LENGTH: 293
                                                                                                                                                                                                                                                                                                                                             Sequence 91758, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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Best Local Similarity 100.0%;
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ORGANISM: Homo sapiens
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RESULT 15
US-09-724-676A-91769
US-09-724-676A-91769
Sequence 91769, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 91769
LENGTH: 293
TYPE: PRI
ORGANISM: Homo sapiens
US-09-724-676A-91769
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 91759
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-676A-91759
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Search completed: January 30, 2003, 14:42:05 Job time : 19 secs
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Pred. No. 1.7e-05;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

				SUMMARIES	
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78	100.0	14	18	AAW21748	Fragment #2 of E33
78	100.0	170	23	ABP42951	Human ovarian anti
78	100.0	318	18	AAW21746	E3330-binding prot
78	100.0	318	19	AAW48894	. Homo sapiens AP en
78	100.0	318	19	AAW52864	Apurinic/apyrimidi
78	100.0	345	21	AAB56610	Human prostate can
78	100-0-	J	19	9 AAW48893	Homo sapiens MGMT-
4.5.	157-7	364-22	133	AAU54366	Propionibacterium
44	56.4	68	21	AAB54099	Human pancreatic c
43	55.1	241	22	AAU47601	Propionibacterium

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Result No.

12 43 55.1 1008 21 AAG53684 13 43 55.1 1065 21 AAG53683 14 42 53.8 115 19 AAY21361 15 42 53.8 38 23 ABB97554 16 42 53.8 38 22 AAB677,64 17 42 53.8 1017 22 AAB95217 18 42 53.8 1146 20 AAW96322 20 42 53.8 1153 15 AAR63264 21 42 53.8 1153 15 AAR63264 22 42 53.8 1153 12 AAR63497 24 25 3.8 1153 22 AAG64497 25 3.8 1153 22 AAG64497 25 3.8 1153 22 AAG64497 26 42 53.8 1153 22 AAG64498 27 42 53.8 1153 22 AAG64498 28 42 53.8 1153 22 AAG64498 29 42 53.8 1153 22 AAG64498 20 42 53.8 1153 22 AAG64498 21 42 53.8 1153 22 AAG64498 22 43 53.8 1153 22 AAG64498 23 44 52.6 1144 22 AAG67743 24 53.8 1153 22 AAG64498 25 3.8 1153 22 AAG64498 26 42 53.8 1153 22 AAG64498 27 42 53.8 1153 22 AAG64498 28 42 53.8 1153 22 AAG64498 29 42 53.8 1153 22 AAG64498 30 42 53.8 1153 22 AAG64498 31 44 52.6 1144 16 AAR772746 31 44 52.6 1144 12 AAR727276 31 44 52.6 1144 12 AAR727276 31 44 52.6 1144 22 AAG64500 36 41 52.6 1144 22 AAG64500 36 41 52.6 1144 22 AAG64500 37 41 52.6 1144 22 AAG64500 38 40 51.3 100 22 AAU31479 39 40 51.3 100 22 AAU31479 40 51.3 134 23 AAB911437 41 40 51.3 134 23 AAB911437 42 40 51.3 134 23 AAB911437 43 40 51.3 134 23 AAB911437 44 51.3 134 23 AAB911437 45 40 51.3 491 22 AAG60811 46 51.3 491 22 AAG60811	•																																		
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Inducible nitric o Sequence encoded b Nitric-oxide-synth Hepatocyte inducible ni Human inducible ni Mouse inducible ni Amino acid sequenc Human inducible ni Amino acid sequenc Human inducible ni Amino acid sequenc Mouse Hairless prote Propionibacterium

E3330-binding protein; Ref-1; microsphere; drug binding factor recovery; styrene-glycidyl methacrylate polymer; protein isolation; Fragment #2 of E3330-binding protein, Ref-1. 02-MAR-1998 (first entry) AAW21748; AAW21748 standard; peptide; 14 AA.

ALIGNMENTS

Human Hairless pro
Novel human diagno
Novel human secret
Novel human secret
Novel human secret
Human ORFX ORF800
Human ORFX protein
Propionibacterium
Rice starch branch
Novel human diagno

Human protein sequ Inducible nitrogen Inducible nitric o Mouse inducible ni Rat inducible nitr

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<pre>wPI; 1997-387634/36.</pre> Isolation and identification of receptors to specific compounds -	Handa H, Kawaguchi H;	(KAWA/) KAWAGUCHI H.	(HAND/) HANDA H.	03. E DO - 1990) 900 F - 00100 Z / .	OR 1999 1000 00 10 0010 001	17-cep-1996. 96.TD-0266711	05-FEB-1997; 97EP-0101821.		06-AUG-1997.	EF/0/900-AZ.	BD707000-30	Synthetic.		protein purification; receptor identification.	styrene-glycidyl methacrylate polymer; protein isolation;	E3330-binding protein; Ref-1; microsphere; drug binding factor rec		Fragment #2 of E3330-binding protein, Ref-1.		02-MAR-1998 (first entry)		AAW21748;		1748 AAW21748 standard; peptide; 14 AA.	LT 1

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RESULT 2
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Matches 14
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3-[(5-(2,3-dimethoxy-6-methyl-1,4-benzoquinonyl)]-2-nonyl-2-propionic acid. Ref-1 was isolated using the method of the invention. The method of the invention is for isolating a substance (S1) that can adhere to a substance (S2) possessing physiological activity from a mixture containing S1. The method comprises contacting the mixture with a microsphere prepared by coupling S2 to a styrene-glycidyl methacrylate polymer through a spacer. The process is useful, e.g., for recovery of drug binding factors (such as proteins) from cell extracts. The process allows easy isolation, purification and identification of receptors to
                                                                                                                                                                                                                                                                                                                                                                                        Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoes; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                using microspheres prepared by coupling the compound, via a spacer, to a styrene-glycidyl methacrylate polymer.
Claim 11; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ovarian antigen HPDVI25, SEQ ID NO:4083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP42951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP42951 standard; Protein; 170
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                                                                                                                                                                                                                               07-JUN-2000; 2000US-209467P.
                                                                                                                                                                                                                                                               07-JUN-2001; 2001WO-US18569
                                                                                                                                                                                                                                                                                               03-JAN-2002
                                                                                                                                                                                                                                                                                                                            WO200200677-A1
                                                                                                                                                                                                                                                                                                                                                                Homo
                                             Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-AUG-2002
                              neurological diseases
                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
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14; Conserv
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Pred. No. 1.1e-05;
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4083; 2922pp; English

Handa H,

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KAWAGUCHI H. Kawaguchi H;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc treating, prognosing or preventing various ovary and/or breast related cd disorders. Such conditions include ovarian cancer and breast cancer, and cd disorders (e.g., infertility, disorders of pregnancy, anovulation, cc disorders (e.g., infertility, disorders of pregnancy, anovulation, cc polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine cd disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic constitution), influence, ovarian cysts, and dysmenorrhoea), endocrine cd immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), cc limmunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), cc respiratory disorders, neurological disorders, gastrointestinal disorders (e.g., anaemia), cardiovascular disorders, complicated and urinary system disorders. Ovarian antigen polypeptides and cc modulate ovarian antigen expression or activity. The polynucleotides may also be used in screening for compounds which complete therapy, chromosome mapping, in the clientification of individuals and in forensic analysis, and the cc polypeptides may be used as food additives or to prepare antibodies conserved a human ovarian antigen of the invention.

Cc Note: The sequence data for this patent did not form part of the printed cast perification, but was obtained in electronic format directly from WIPO at the pulpo with the printed of the first pulpo with the printed of the first pulpo with the printed of the first pulpo with the pulpo wit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotides, antibodies against human ovarian antigens, and the of ovarian antigen polynucleotides and polypeptides in diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                         styrene-glycidyl methac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW21746 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                          17-SEP-1996;
05-FEB-1996;
                                                                                                                                                                                                                              05-FEB-1997;
                                                                                                                                                                                                                                                                           06-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                         styrene-glycidyl methacrylate polymer; protein isolation; protein purification; receptor identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E3330-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW21746;
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                                                                                                                                                            96JP-0018827
                                                                                                                                                                               96JP-0266711.
                                                                                                                                                                                                                                97EP-0101821.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ref-1; microsphere; drug binding factor recovery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318
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Pred. No.
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0.00014;
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                                                                                                                                           protecting agents, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-[(5-(2),3-dimethoxy-6-methyl-1,4-benzoquinonyl)]-2-nonyl-2-propionic acid. This sequence was isolated using the method of the invention. The method of the invention is for isolating a substance (S1) that can adhere to a substance (S2) possessing physiological activity from a mixture containing S1. The method comprises contacting the mixture with a microsphere prepared by coupling S2 to a styrene-glycidyl methacrylate polymer through a spacer. The process is useful, e.g., for recovery of drug binding factors (such as proteins) from cell extracts. The process allows easy isolation, purification and identification of receptors to
             The sequence is that encoding the APE gene which was used in the construction of a fusion protein of the DNA repair proteins 0-6-methylguanine-DNA methyltransferase (MGMT) and AP endonuclease (APE). It can be used for protecting cells (especially bone marrow cells) against DNA damaging agents such as chemotherapeutic agents used in tumour therapy and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolation and identification of receptors to specific using microspheres prepared by coupling the compound, to a styrene-glycidyl methacrylate polymer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specific compounds.
 conjunction with chemotherapy
                                                                                                                 Disclosure; pl15-116; 150pp; English
                                                                                                                                                                                                                                              Kelley
                                                                                                                                                                                                                                                                                                      25-OCT-1996;
                                                                                                                                                                                                                                                                                                                                24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                        WO9817684-A2
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGMT; APE; DNA repair
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                                                                                                                                                                                                                                                                        (ADRE-) ADVANCED RES & TECHNOLOGY INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAGEGPALYEDPPD 14
                                                                                                                                       fusion proteins comprising 2 DNA repair proteins - used tecting cells against DNA damage, e.g. by chemotherapeut: nts, or for treating DNA-repair-defective human diseases
                                                                                                                                                                                                   1998-271785/24.
DB; AAV32543.
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                                                                                                                                                                                                                                            Williams
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                                                                                                                                                                                                                                                                                                    96US-0029308
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                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; fusion protein;
methyltransferase.
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Pred. No.
  to facilitate
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. 0.00026;
ches 0;
                                                                                                                                       chemotherapeutic
  the use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP endonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 318;
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increased doses
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                                                The present sequence represents an apurinic/apyrimidinic endonuclease (APE). Levels of APE in dysplasia, caicinoma in situ and squamous cell carcinomas of the cervix and prostate are substantially elevated, relative to controls. A method for identifying a premalignant or malignant condition in a human subject comprises determining the level of APE in cells from the subject, where an elevated level of APE, as compared to the APE level in corresponding normal cells, indicates a premalignant or malignant condition. APE levels can be used in the diagnosis and therapy of tumours. They can also be used for detecting, inducing, or inhibiting apoptosis in cells, e.g. for treating T-cells infected with HIV or detecting apoptosis in cells that have been subjected to chemo-, radio- or gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of chemotherapy. They can provide added protection to cells by providing RPs which recognise different types of DNA lesions. In addition, the FPs can be used in the treatment of DNA-repair-defective human diseases, e.g. Xeroderma Plgmentosum, Ataxia Telangiectasia, Cockayne's syndrome, Bloom's syndrome, Fanconi's anaemia, Parkinson's disease and other neurodegenerative diseases including amyotrophic lateral sclerosis, Alzheimer's disease and other age related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of apurinic/apyrimidinic endonuclease - 1 for the diagnosis and therapy of tumours, or or inhibiting apoptosis in cells
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duguid JR, Eble JN,
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11-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apurinic/apyrimidinic APE level; diagnosis;
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DB; AAV21204.
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   318
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Pages 131-132; 166pp; English.
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96US-0019561.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endonuclease; APE; identification;
therapy; tumour; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kelley MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Pred. No.
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0.00026;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for developing products for detecting, inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     premalignancy;
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Query Match Best Local Similarity

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Score 78; Pred. No.

DB 19; 0.00026;

Length 318;

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ID AAB5
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                                                     Matches
                                                             Query Match
Best Local :
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                                                                                                                   proteins, called prostate cancer antigens, given in AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                             Sequence
                                                                                                                                                                                                                                                                  Claim 11; Page 1600; 2338pp; English.
                                                                                                                                                                                                                                                                                                Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease.
                                                                                                                                                                                                                                              AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                        disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAF15813.
                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate cancer antigen
                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                 Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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           64
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                      1 AAGEGPALYEDPPD 14
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           AAGEGPALYEDPPD 77
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                                                              Similarity
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ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                 Ruben SM
                                                                                            345 AA;
                                                     Conservative
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                                                            Score 78;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein sequence SEQ ID NO:1188.
                                                   Mismatches
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                                                             0.00028;
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                                                                     Length 345;
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                                                                                                                                                    RESULT 8
AAU54366
ID AAU5
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                                                                                                              Matches
                                                                                                                                Query Match
AAU54366;
                  AAU54366 standard;
                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                              Kelley M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-OCT-1997;
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                                                                       243
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                                                                                                                        Local
                                                                      AAGEGPALYEDPPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
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                                                                                                              14;
                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                               Williams
                                                                                                                                                      524 AA;
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The sequence is that of fusion protein of the DNA repair proteins 0-6-methylguanine-DNA methyltransferase (MGMT) and AP endonuclease (APE). It can be used for protecting cells (especially bone marrow cells) against DNA damaging agents such as chemotherapeutic agents used in tumour therapy and can be used in conjunction with chemotherapy to facilitate the use of increased doses of chemotherapy. They can provide added protection to cells by providing RPs which recognise different types of DNA lesions. In addition, the FPs can be used in the treatment of DNA-repair-defective human diseases, e.g. Xeroderma Pigmentosum, Ataxia Telangicctasia, Cockayne's syndrome, Bloom's syndrome, Fanconi's anaemia, Parkinson's disease and other neurodegenerative diseases including amyotrophic lateral sclerosis, Alzheimer's disease and other age related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; p108-110; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion proteins comprising 2 DNA repair proteins - used for protecting cells against DNA damage, e.g. by chemotherapeutic agents, or for treating DNA-repair-defective human diseases
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                                                                                                                                                                       1 AAGEGPALYEDPPD 14
                                                                                                                                                                                                                                                       Conservative
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208..524
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Protein;
                                                                                                                                          256
                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "APE"
  364
                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                  Score 78;
Pred. No.
  A
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                    0.00042;
hes 0;
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                                                                                                                                                                                                                                                                                                         Length 524;
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RESULT 9
AAB54099
ID AAB5
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AC AAB5
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Best Local Similarity
"---hes 8; Conserve
                                                                                                                                                                                                                                                                                Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the CC presence or absence of P. acnes in a patient comprises contacting a gener that binds to the proteins of the invention CC and determining the amount of bound protein in the sample. The CC sample with a binding agent that binds to the production of antibodies specific for P. acnes proteins. These antibodies can be used to CC downregulate expression and activity of P. acnes polypeptides and CC diagnostic agents for determining P. acnes protein some proteins may also be used as CC diagnostic agents for determining P. acnes proteins. The antibodies may also be used as CC diagnostic agents for determining P. acnes protein, by CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO of the printed of the protein in the printed specification, but was obtained in electronic format directly from WIPO of the printed specification.
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
 AAB54099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccinating against and treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-2001
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                                   AAB54099 standard; Protein; 68
                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L'maisonneuve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky YAW,
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                                                                                                                               200 GESPYTGEDPPD 211
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                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                  GEGPALYEDPPD 14
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                                                                                                                                                                                                         Conservative
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e J, Zhang Y,
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                                                                                                                                                                                                                         57.7%;
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Jen S, Carter D;
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                                                                                                                                                                                                                       Score 45;
Pred. No.
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                                                                                                                                                                                                                     DB 45;
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RESULT 10 AAU47601 ID AAU47

AAU47601 standard; Protein;

241 AA.

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                                                                                                                                                                                                                                          CC AAC98773 to AAC99231 encode the human pancreatic cancer associated CC proteins, called pancreatic cancer antigens, given in AAB54008 to CC AAB54466. The human pancreatic cancer antigens have cytostatic, CC neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, CC synaecological, cardiant and antiinflammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for CC preventing, treating, or ameliorating a medical condition or in assays CC for diagnosing a pathological condition or a susceptibility to one in a CC subject. Binding partners to the proteins and the activity of the CC proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer. CC Agonists and antagonists to the antigens can be screened for The CC pancreatic cancer antigen polynucleotides can be used to design nucleic candiagnostic methods. The proteins can be used to design nucleic candiagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including continuous control control can be used to generate antibodies of the proteins can be used to generate antibodies of the proteins can be used to generate antibodies can be used to generate antibodies and the cancer used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proteins can be used to treat or prevent neural, immune system, muscular, continuous can be used to cardiovascular, renal or continuous can be used to cardiovascular, renal or continuous can be used to cardiovascular, renal or cardiovascular, renal or continuous can be used to cardiovascular, renal or cardiovascular, re
                                                                                     Query Match
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Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAR-2001
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                                                                                                                                                                                                                              sequences
39
                          1 AAGEGPALYEDPP 13
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AAGQEPCXLEDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pancreatic cancer antigen protein sequence SEQ
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                                                                                     8; Conserv
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                                                                                                                                                                                                                              used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                                                68 AA;
                                                                                        Conservative
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51
                                                                                                           56.4%;
                                                                                     Score 44; DB Pred. No. 12; 1; Mismatches
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                                                                                                                                                                                                                              present invention.
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RESULT 11
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                                                                                                                                                                                                                                                         Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in CC the treatment, prevention and diagnosis of medical conditions caused by CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, used in cc pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC P. acnes is also involved in infections of bone, joints and the central CC entrous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the CC presence or absence of P. acnes in a patient comprises contacting a CC sample with a binding agent that binds to the proteins of the invention CC and determining the amount of bound protein in the sample. The CC specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and CC downregulate expression and activity of P. acnes polypeptides and CC diagnostic agents for determining P. acnes presence, for example, by CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed constitution, but was obtained in electronic format directly from WIPO at figure and polypeptides and consideration, but was obtained pot_sequences.
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Matches 8
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful
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 AAG53685 standard; Protein; 999
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hybridisation assay; genetic mapping; gene expression control; promoter;
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99US-0134216.
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RESULT 12
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6 GPGPSLHQLPPD
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3; Mismatches
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RESULT 13
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                                                             Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
    EP1033405-A2.
                                 Arabidopsis thaliana.
                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 68370.
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                                                                                                                                                                                         AAG53683;
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Pred. No. 2.6e+02;
3; Mismatches 2;
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23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
                                                                                      Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; biquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M; neurofilament-F; presenilin I; presenilin II; cellular tumour antigen; glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1; bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY21361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY21361 standard; Protein;
                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                   Human HUPF-I mutant protein fragment 13.
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22 GPGPSLHQLPPD 433
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99US-0159295.
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99US-0157117.
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58.3%;
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Pred. No. 2.7e+02;
3; Mismatches 2;
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9905-01445422
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9905-01443624
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WO9845322-A2

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RESULT 15
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Best Local
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protein-C
                                                                            Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy; neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift
WO200222660-A2
                               Homo sapiens.
                                                              expressed sequence
                                                                                                                                               Novel human protein SEQ ID NO:
                                                                                                                                                                                  27-JUN-2002
                                                                                                                                                                                                                   ABB97554;
                                                                                                                                                                                                                                                ABB97554 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Figure 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-APR-1998;
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(ROYA-) ROYAL NETHERLANDS
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DB; AAX75768.
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HMGP-C) and neuroendocrine specific protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 AA;
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                                                              tag.
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Pred. No.
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Search completed: January 30, 2003, 14:37:38 Job time: 37 secs

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                                                                                                                                      The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate the immune system e.g. to treat multiple sclerosis, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. theumatoid arthritis, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a protein of the invention.
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 822; 509pp; English.
                                                                                                                                                                                                                                                                                                                         An isolated polynucleotide for treating diseases associated with encoded polypeptide such as cancer and multiple sclerosis -
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N-PSDB; ABN32740.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
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SAGEGPVIYVHP
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                                                      Similarity 7; Conserva
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                                                       Conservative
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Wehrman T,
                                                                   53.8%;
58.3%;
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                                                       Mismatches
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Pred. No. 1.4e+02;
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Drmanac RT;
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Listing first 45 summaries
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Perfect score:
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    protein search, using
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1: sp_archea:*
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3: sp_fungl:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:*
9: sp_page:*
10: sp_plant:*
11: sp_rodent:
12: sp_vtrus:*
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(without alignments)
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Compugen Ltd.
O97870 ateles belz
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O92272 cricetulus
O72205 hepatitis c
O72206 hepatitis c
O72208 hepatitis c
O72208 hepatitis c
O72209 hepatitis c
O72210 hepatitis c
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1017	945	583	392	331	303	186	186	157	226	3104	1157	1006	224	186	186	186	186	186	186	186	121	121	121	612	328	438	186	186
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Q9 Н9В8	Q9N175	Q9VYH5	Q9Z1Z6	Q92QA9	Q9UBE5	Q9IXUS	Q9IXU7	Q95MM7	Q9D492	Q04846	Q8TK13	Q8RXU9	073450	Q9IXX5	Q9IXX6	Q91XX7	091XX8	Q9IXY1	Q9IXY2	Q9IXZO	Q9WG87	Q9WGB5	Q9WG82	Q9X0L0	Q8YC05	Q54823	Q9IXV4	8AXI60
homo	Q9n175 ovis aries	Q9vyh5 drosophila	9	စ	Q9ube5 homo sapien	5 hepatitis	-	Q95mm7 equus cabal	Q9d492 mus musculu	Q04846 corynebacte	Q8tk13 methanosarc	Q8rxu9 arabidopsis	-	19		tis	hepatit	l hepatitis	hepatitis		hepatitis	hepatitis	hepatitis	Q9x010 thermotoga	Q8yc05 brucella me	9	4 hepatitis	Q91xv8 hepatitis c

ALIGNMENTS

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RESULT 1
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APE-MHY7 to 2q; AR-GLA-F8C to the X chromosome.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF66468; AAD17542.1; -.
HSSP; P27695; BISIX.
InterPro; IPR000097; APendonclsel.
InterPro; IPR005135; EXO_endo_phos.
Pfam; PF03372; EXO_endo_phos.
Pfam; PF03372; EXO_endo_phos; 1.
PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
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097870;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2002 (TrEMBLrel. 21,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Ateles.
NCBI_TaxID=118643;
                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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1 AAGEGPALYEDPPD 14
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1 AAGEGPSLYEDPPD 14
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92.9%;
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Last sequence update)
Last annotation update)

    Mismatches

                                                                                                                                                                                  Score 75; DB 6;
Pred. No. 3.1e-05;
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Best Local S
Matches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004442; EXODNASe_III.
InterPro; IPR004808; EXOLII_xth.
InterPro; IPR005135; EXO_endo_phos.
Pfam; PF03372; EXO_endo_phos; 1.
TIGRPAMS; TIGR00195; exoDNASe_III; 1.
TIGRPAMS; TIGR00633; xth; 1.
PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
PROSITE; PS00727; AP_NUCLEASE_F1_2; 1.
PROSITE; PS00728; AP_NUCLEASE_F1_3; 1.
InterPro; IPR000097; APendoncisel.
InterPro; IPR00442; EXONNASe_III.
InterPro; IPR004480#; EXOIII_xth.
InterPro; IPR005135; EXO_endo_phos.
Pfam; PF03372; EXO_endo_phos; 1.
TIGRFAMS; TIGR00195; eXONASe_III; 1.
TIGRFAMS; TIGR00633; xth; 1.
PROSITE; PS00726; AP_NUCLEASE_F1_1; 1.
                                                                                                                                                                                                                  Cricetulus griseus ((Eukaryota; Metazoa; (Mammalia; Eutheria; Cricetulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q99PF3;
                                                                                                                                                                                                                                                                  0922J2;
01-MAY-1999 (TrEMBLrel. 10, Created;
01-MAY-1999 (TrEMBLrel. 10, Last sec
01-JUN-2002 (TrEMBLrel. 21, Last and
Apurinic/apyrimidinic endonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                       "Molecular cloning, sequence and structure analysis apurinic/apyrimidinic endonuclease (chapEl) gene."; Mutat. Res. 435:215-224(1999).
EMBL; AF056934; AAD02702.1; -.
HSSP; P27695; 1E9N.
                                                                                                                                                                                                                                                                                                                                 Q9Z2J2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APEX (Fragment).
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                                                                                                                                                 Purohit S., Arenaz P.;
                                                                                                                                                             MEDLINE=20075118; PubMed=10606812;
                                                                                                                                                                                                       NCBI_TaxID=10029;
                                                                                                                                                                          FISSUE=OVARY;
                                                                                                                                                                                   SEQUENCE FROM N.A.
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13; Conserv
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                                                                                                                                                                                                                          (Chinese hamster).
; Chordata; Craniata; Vert
; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              94.9%;
 _NUCLEASE_F1_1; 1.
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17,
21,
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Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
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RESULT 5
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ID 0722
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Matches 8
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Best Local Similarity 85.3
Matches 12; Conservative
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PROSITE; PS00728; AP
Endonuclease.
Endonuclease.
317 AA;
                                                                                        O72206 PRELIMINARY;
O72206;
O72206;
O1-AUG-1998 (TrEMBLrel. 07, Cre
O1-AUG-1998 (TrEMBLrel. 19, Las
O1-DEC-2001 (TrEMBLrel. 19, Las
Genome polyprotein [Contains: e
(NS1)] (Fragment).
Hepatitis C virus
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072205;
01-AUG-1998
01-AUG-1998
01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome polyprotein (NS1)] (Fragment). Hepatitis C virus.
                                    Viruses; ssRNA positive-strand Hepacivirus. NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01539; HCV_env; Pfam; PF01560; HCV_NS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand Hepacivirus.
  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD186062; HCV_NS1; 1
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Similarity 57.1%;
8; Conservative
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Gremblrel.
Gremblrel.
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85.7%;
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s: envelope glycoprotein
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                                                                              viruses,
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                                                                                                                                                      Query Match
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Best Local
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STRAIN-ANTI-D RECIPIENT 1;

STRAIN-ID RECIPIENT 1;

MEDLINE-98241727; PubMed-9573256;

MCAllistear J. Casino C., Davidson F., Power McAllistear J. Casino C., Davidson F., Power Simmonds P., Smith D.B.;

"Long-term evolution of the hypervariable regions of the common-source-infected cohort.";

"Long-term evolution of the hypervariable regions of the common-source-infected cohort.";

"Long-term evolution of the hypervariable regions of the cohort.";

"Long-term evolution of the hypervariable regions of the cohort.";

"Long-term evolution of the hypervariable regions of the cohort.";

J. Virol. 72:4893-4905(1998).

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AF055774; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AAC17270.1;

-1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPIEMBL; AAC17270.1;

-1- SIMILARITY: TO H
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepacivirus.
NCBI_TaxID-11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome polyprotein [Contains: envelope (NS1)] (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---- SIMILARITY: TO HEPÁTITIS C VIRUS EMBL; AROS6773; AAC17269 L; --
InterPro; IPR002531; HCV_env.
InterPro; IPR002531; HCV_NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01539; HCV_env; 1. Pfam; PF01560; HCV_NS1; 1. ProDom; PD186062; HCV_NS1; 1.
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J. Virol. 72:4893-4905(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ANTI-D RECIPIENT 1;
MEDLINE-98241727; PubMed-9573256;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simmonds P., Smith D.B.;
    101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 AQGWGPITYAEPPD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                               μ
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AQGWGPITYAEPPD 114
                                                                       AAGEGPALYEDPPD 14
                                                                                                                                                           Similarity
8; Conserv
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8; Conservative
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121 AA;
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121 AA;
                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                      121
13254 MW;
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13281 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.7%;
57.1%;
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57.1%;
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                                                                                                                                                                                            Score 45; I
Pred. No. 5
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                                                                                                                                                                                                                                                                                                                      B04523A965CA1367 CRC64;
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                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Power J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
5.9;
                                                                                                                                                                                                DB 12;
5.9;
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                                                                                                                                                                                                                                  Length 121;
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                                                                                                                                                      Gaps
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RESULT 7
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Best Local (
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"Long-term evolution of the hypervariable re
in a common-source-infected cohort.";

J. Virol. 72:4893-4905(1998).

-!- SIMILARITY: TO HEPATITIS C VIRUS ENVELOP
EMBL; AF056775; AAC17271.1;
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InterPro; IPR002519; HCV_env.
InterPro; IPR002531; HCV_NS1.
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072209; O1-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEG-2001 (TrEMBLrel. 19, Last annotation updat Genome polyprotein [Contains: envelope glycoprote (NSI)] (Fragment).
Hepatitis C virus.
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ANTI-D RECIPIENT 1;
MEDLINE-98241727; PubMed-9573256;
MEDLINE-98241727; PubMed-9573256;
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NON_TER
SEQUENCE
                                                                                                    SEQUENCE FROM N.A.
STRAIN-ANTI-D RECIPIENT 1;
MEDLINE-98241727; PubMed-9573256;
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Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, Hepacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01539; HCV_env; 1. Pfam; PF01560; HCV_NS1; 1. ProDom; PD186062; HCV_NS1; 1.
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NCBI_TaxID=11103;
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                      Pfam; PF01539; HCV_env; 1. Pfam; PF01560; HCV_NS1; 1.
                                                              InterPro; IPR002519; HCV_env.
InterPro; IPR002531; HCV_NS1.
                                                                                                                                                                                                                McAllister J., Casino C., Davidson Simmonds P., Smith D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coat protein; Envelope protein; Polyprotein; Transmembrane.
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8; Conserv
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13284 MW;
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57.18;
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Pred. No. 5
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                                                                                                                             ENVELOPE
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                                                                                                                                                                                                                                    Power J.,
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                                                                                                                                                                                                                                                                                                                                                                                      DNA stage;
                                                                                                                             GLYCOPROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
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                                                                                                                                                                                            of hepatitis C virus
                                                                                                                                                                                                                                    Lawlor
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                                                                                                                                                                                                                                                                                                                                                                                        Flaviviridae;
                                                                                                                                                                                                                                    (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GP68) (GP70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GP68) (GP70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E., Yap
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STRAIN-ANTI-D RECIPIENT 1;

MEDLINE-98241727; pubMed=9573256;

McAllister J., Casino C., Davidson F., Pow Simmonds P., Smith D.B.;

"Long-term evolution of the hypervariable in a common-source-infected cohort.";

J. Virol. 72:4893-4905(1998).
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01-AUG-1998 (TrEMBLrel.
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Pfam; PF01560; HCV_NS1; 1.
ProDom; PD186062; HCV_NS1; 1.
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses,
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NCBI_TaxID=11103;
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Alter H.J.;
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STRAIN-ANTI-D RECIPIENT 1;
MEDLINE-98241727; PubMed-9573256;
MCAllister J., Casino C., Davidson
Simmonds P., Smith D.B.;
                                                                          Polyprotein; Transmembrane.
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NON_TER 186 186
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EMBL; AF246078; AAF66377.1; -.
InterPro; IPR002519; HCV_env.
InterPro; IPR002531; HCV_NS1.
                                                                                                                                                                                          viral quasispecies.";
science 288:339-344(2000).
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InterPro; IPR002519; HCV_env.
InterPro; IPR002519; HCV_NS1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01560; HCV_NS1; 1.
ProDom; PD186062; HCV_NS1; 1.
Coat protein; Envelope protein; Gl
Polyprotein; Transmembrane.
NON_TER 186 186
NON_TER 186 186
"The outcome of acute hepatitis C viral quasispectes.";
Science 288:339-344(2000).
-I- SIMILARITY: TO HEPATITIS C VII
EMBL; AF246085; AAF66384.1; -.
InterPro; IPR002519; HCV_env.
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O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genome polyprotein (Contains: envelope glycoprotein (NS1)] (Fragment).

Honatitis C virus.
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MEDLINE-20230065; PubMed-10764648;
Farci P., Shimoda A., Colana A., Diaz
Strazzera A., Chien D.Y., Munoz S.J.,
Alter H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus. Viruses; ssRNA positive-strand Hepacivirus.
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Farci P., Shimoda A., Colana A., Diaz G., Peddis (
Strazzera A., Chien D.Y., Munoz S.J., Balestrieri
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186 AA;
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Pred. No. 9
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Pfam; PF01560; HCV_NS1; 1.
ProDom; PD186062; HCV_NS1; 1.
Coat protein; Envelope protein; Gl
Polyprotein; Transmembrane.
NON_TER 186 186
SEQUENCE 186 AA; 20280 MW; F0:
                                                                                                                                                                                                                                                                                        viral quasispecies.";
Science 288:339-344(2000).
Science 288:339-344(2000).
Interpro; TPR002519; HCV_env.
Interpro; IPR002519; HCV_NS1.
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Q9IXW1 PRELIMINARY; PRT; 186 AA.
Q9IXW1;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genome polyprotein [Contains: envelope glycoprotein (NS1)] (Fragment).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genome polyprotein (Contains: envelope glycoprotein
                                                                                                                                                                                                                  MEDLINE=20230065; PubMed=10764648; Farci P., Shimoda A., Colana A., Diaz Strazzera A., Chien D.Y., Munoz S.J.,
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Pfam; PF01560; HCV_NS1; 1.
ProDom; PD186062; HCV_NS1; 1.
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Hepatitis C virus.
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57.1%;
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OCCORDARA RADARA DARA RADARA R
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RI Science 288:339-344(2000).
CC -!-SMILARTY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR HITTOPY: IPRO02519; HCV_env.
DR InterPro; IPRO02519; HCV_env; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NS1; 1.
DR Probom; PD186062; HCV_NS1; 1.
DR Probom; PD186062; HCV_NS1; 1.
COAT protein; Envelope protein; Glycoprotein; Nonstructural protein; MON_TER 186 186
FT NON_TER 186 AA; 20293 MW; B4D07F7DEF4EB197 CRC64;
                                                                                                                                                                                                                                                                                                                                                  Query Match 57.7%;
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20230065; PubMed=10764648;
Farci P., Shimoda A., Coiana A., Diaz G., Peddis G., Melpolder J.C.,
Strazzera A., Chien D.Y., Munoz S.J., Balestrieri A., Purcell R.H.,
Alter H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TaxID=11103;
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STRAIN-P10;
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| | || | :|||
                                                                                                                                                                                                                                                                                                                                                       score 45; DB 12; Length 186;
Pred. No. 9.5;
1; Mismatches 5; Indels
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